

# Sequence Listing

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Botstein, David  
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Eaton, Dan L.  
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Fong, Sherman  
Gao, Wei-Qiang  
Goddard, Audrey  
Godowski, Paul J.  
Grimaldi, Christopher J.  
Gurney, Austin L.  
Hillan, Kenneth J.  
Pan, James  
Paoni, Nicholas F.  
Roy, Margaret Ann  
Smith, Victoria  
Stewart, Timothy A.  
Tumas, Daniel  
Watanabe, Colin K.  
Williams, P. Mickey  
Wood, William I.

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Trp	Thr	Arg	Lys	Gly	Lys	Leu	Lys	Ile	Glu	Asp	Ile	Thr	Asp	Lys
				20					25					30

Tyr	Ile	Phe	Ile	Thr	Gly	Cys	Asp	Ser	Gly	Phe	Gly	Asn	Leu	Ala
				35					40					45

Ala	Arg	Thr	Phe	Asp	Lys	Lys	Gly	Phe	His	Val	Ile	Ala	Ala	Cys
				50					55					60

Leu	Thr	Glu	Ser	Gly	Ser	Thr	Ala	Leu	Lys	Ala	Glu	Thr	Ser	Glu
				65					70					75

Arg	Leu	Arg	Thr	Val	Leu	Leu	Asp	Val	Thr	Asp	Pro	Glu	Asn	Val
				80					85					90

Lys	Arg	Thr	Ala	Gln	Trp	Val	Lys	Asn	Gln	Val	Gly	Glu	Lys	Gly
				95					100					105

Leu	Trp	Gly	Leu	Ile	Asn	Asn	Ala	Gly	Val	Pro	Gly	Val	Leu	Ala
				110					115					120

Pro	Thr	Asp	Trp	Leu	Thr	Leu	Glu	Asp	Tyr	Arg	Glu	Pro	Ile	Glu
				125					130					135

Val	Asn	Leu	Phe	Gly	Leu	Ile	Ser	Val	Thr	Leu	Asn	Met	Leu	Pro
				140					145					150

Leu	Val	Lys	Lys	Ala	Gln	Gly	Arg	Val	Ile	Asn	Val	Ser	Ser	Val
				155					160					165

Gly	Gly	Arg	Leu	Ala	Ile	Val	Gly	Gly	Gly	Tyr	Thr	Pro	Ser	Lys
				170					175					180

Tyr	Ala	Val	Glu	Gly	Phe	Asn	Asp	Ser	Leu	Arg	Arg	Asp	Met	Lys
				185					190					195



Ala	Phe	Gly	Val	His	Val	Ser	Cys	Ile	Glu	Pro	Gly	Leu	Phe	Lys
				200					205					210
Thr	Asn	Leu	Ala	Asp	Pro	Val	Lys	Val	Ile	Glu	Lys	Lys	Leu	Ala
				215					220					225
Ile	Trp	Glu	Gln	Leu	Ser	Pro	Asp	Ile	Lys	Gln	Gln	Tyr	Gly	Glu
				230					235					240
Gly	Tyr	Ile	Glu	Lys	Ser	Leu	Asp	Lys	Leu	Lys	Gly	Asn	Lys	Ser
				245					250					255
Tyr	Val	Asn	Met	Asp	Leu	Ser	Pro	Val	Val	Glu	Cys	Met	Asp	His
				260					265					270
Ala	Leu	Thr	Ser	Leu	Phe	Pro	Lys	Thr	His	Tyr	Ala	Ala	Gly	Lys
				275					280					285
Asp	Ala	Lys	Ile	Phe	Trp	Ile	Pro	Leu	Ser	His	Met	Pro	Ala	Ala
				290					295					300
Leu	Gln	Asp	Phe	Leu	Leu	Leu	Lys	Gln	Lys	Ala	Glu	Leu	Ala	Asn
				305					310					315

Pro Lys Ala Val

<210> 11  
 <211> 2720  
 <212> DNA  
 <213> Homo sapiens

<400> 11  
 gcgggctggt gacggogctg cgatggctgc ctgcgagggc aggagaagcg 50  
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 gccccttggg ccgtcgccac cactgtagtc atgtaccac cgccgccgcc 150  
 gccgcctcat cgggaacttca tctcggtgac gctgagcttt ggcgagagct 200  
 atgacaacag caagagttgg cggcggcgct cgtgctggag gaaatggaag 250  
 caactgtcga gattgcagcg gaatatgatt ctcttctctc ttgcctttct 300  
 gcttttctgt ggactcctct tctacatcaa cttggctgac cattggaaag 350  
 ctctggcttt caggctagag gaagagcaga agatgaggcc agaaattgct 400  
 ggggttaaac cagcaaacc acccgtctta ccagctcctc agaaggcgga 450  
 caccgaccct gagaacttac ctgagatttc gtcacagaag acacaaagac 500  
 acatccagcg gggaccacct cacctgcaga ttagaccccc aagccaagac 550  
 ctgaaggatg ggaccagga ggaggccaca aaaaggcaag aagcccctgt 600  
 ggatccccgc ccggaaggag atccgcagag gacagtcac agctggaggg 650

gagcggatgat cgagcctgag cagggcaccg agctcccttc aagaagagca 700  
 gaagtgccca ccaagcctcc cctgccaccg gccaggacac agggcacacc 750  
 agtgcattctg aactatcgcc agaagggcgt gattgacgtc ttcttgcattg 800  
 catggaaagg ataccgcaag tttgcatggg gccatgacga gctgaagcct 850  
 gtgtccaggt ccttcagtga gtgggttggc ctcggtctca cactgatcga 900  
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 aacctgtttg agagcacgat ccgcatcctg ggggggctcc tgagtgccta 1050  
 ccacctgtct ggggacagcc tcttctctgag gaaagctgag gatcttggaa 1100  
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 cactgtggcc gaggtgacca gcattcagct ggagttccgg gagctctccc 1250  
 gtctcacagg ggataagaag tttcaggagg cagtggagaa ggtgacacag 1300  
 cacatccacg gcctgtctgg gaagaaggat gggctggtgc ccatgttcat 1350  
 caataccac agtggcctct tccccacct gggcgtattc acgctgggcg 1400  
 ccagggccga cagctactat gactacctgc tgaagcagtg gatccagggc 1450  
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 accggcagat ggagacgggg ctgagtcccg agatcgtgca cttcaacctt 1750  
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 ttcagccgat tcacacgggt cccctcgggt ggctattctt ccatcaacaa 1950  
 tgtccaggat cctcagaagc ccgagcctag ggacaagatg gagagcttct 2000  
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 aacctgctca gcctggacgc ctacgtgttc aacaccgaag cccacctct 2100

gcctatctgg acccctgcct aggggtggatg gctgctgggtg tggggacttc 2150  
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 cagtcttgggt gtgatgcggg gtgggctggg ccgctggagc ctccgctgc 2350  
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 ggtgaccgag tggacagccc aggggtgcagc tctgcccggg ctctggaagc 2500  
 ctcagatgtc cccaatccaa gggctctggag gggctgccgt gactccagag 2550  
 gcctgagggt ccagggctgg ctctggtggt tacaagctgg actcagggat 2600  
 cctcctggcc gccccgcagg gggcttggag ggctggacgg caagtccgtc 2650  
 tagctcagg gcccctccag tggaatgggt cttttcgggt gagataaaaag 2700  
 ttgatttgct ctaaccgcaa 2720

<210> 12  
 <211> 699  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> TRANSMEM  
 <222> 21-40 and 84-105  
 <223> Transmembrane Domain (type II)

<400> 12  
 Met Ala Ala Cys Glu Gly Arg Arg Ser Gly Ala Leu Gly Ser Ser  
 1 5 10 15  
 Gln Ser Asp Phe Leu Thr Pro Pro Val Gly Gly Ala Pro Trp Ala  
 20 25 30  
 Val Ala Thr Thr Val Val Met Tyr Pro Pro Pro Pro Pro Pro  
 35 40 45  
 His Arg Asp Phe Ile Ser Val Thr Leu Ser Phe Gly Glu Ser Tyr  
 50 55 60  
 Asp Asn Ser Lys Ser Trp Arg Arg Arg Ser Cys Trp Arg Lys Trp  
 65 70 75  
 Lys Gln Leu Ser Arg Leu Gln Arg Asn Met Ile Leu Phe Leu Leu  
 80 85 90  
 Ala Phe Leu Leu Phe Cys Gly Leu Leu Phe Tyr Ile Asn Leu Ala  
 95 100 105

Asp	His	Trp	Lys	Ala	Leu	Ala	Phe	Arg	Leu	Glu	Glu	Glu	Gln	Lys		110	115	120
Met	Arg	Pro	Glu	Ile	Ala	Gly	Leu	Lys	Pro	Ala	Asn	Pro	Pro	Val		125	130	135
Leu	Pro	Ala	Pro	Gln	Lys	Ala	Asp	Thr	Asp	Pro	Glu	Asn	Leu	Pro		140	145	150
Glu	Ile	Ser	Ser	Gln	Lys	Thr	Gln	Arg	His	Ile	Gln	Arg	Gly	Pro		155	160	165
Pro	His	Leu	Gln	Ile	Arg	Pro	Pro	Ser	Gln	Asp	Leu	Lys	Asp	Gly		170	175	180
Thr	Gln	Glu	Glu	Ala	Thr	Lys	Arg	Gln	Glu	Ala	Pro	Val	Asp	Pro		185	190	195
Arg	Pro	Glu	Gly	Asp	Pro	Gln	Arg	Thr	Val	Ile	Ser	Trp	Arg	Gly		200	205	210
Ala	Val	Ile	Glu	Pro	Glu	Gln	Gly	Thr	Glu	Leu	Pro	Ser	Arg	Arg		215	220	225
Ala	Glu	Val	Pro	Thr	Lys	Pro	Pro	Leu	Pro	Pro	Ala	Arg	Thr	Gln		230	235	240
Gly	Thr	Pro	Val	His	Leu	Asn	Tyr	Arg	Gln	Lys	Gly	Val	Ile	Asp		245	250	255
Val	Phe	Leu	His	Ala	Trp	Lys	Gly	Tyr	Arg	Lys	Phe	Ala	Trp	Gly		260	265	270
His	Asp	Glu	Leu	Lys	Pro	Val	Ser	Arg	Ser	Phe	Ser	Glu	Trp	Phe		275	280	285
Gly	Leu	Gly	Leu	Thr	Leu	Ile	Asp	Ala	Leu	Asp	Thr	Met	Trp	Ile		290	295	300
Leu	Gly	Leu	Arg	Lys	Glu	Phe	Glu	Glu	Ala	Arg	Lys	Trp	Val	Ser		305	310	315
Lys	Lys	Leu	His	Phe	Glu	Lys	Asp	Val	Asp	Val	Asn	Leu	Phe	Glu		320	325	330
Ser	Thr	Ile	Arg	Ile	Leu	Gly	Gly	Leu	Leu	Ser	Ala	Tyr	His	Leu		335	340	345
Ser	Gly	Asp	Ser	Leu	Phe	Leu	Arg	Lys	Ala	Glu	Asp	Phe	Gly	Asn		350	355	360
Arg	Leu	Met	Pro	Ala	Phe	Arg	Thr	Pro	Ser	Lys	Ile	Pro	Tyr	Ser		365	370	375
Asp	Val	Asn	Ile	Gly	Thr	Gly	Val	Ala	His	Pro	Pro	Arg	Trp	Thr		380	385	390
Ser	Asp	Ser	Thr	Val	Ala	Glu	Val	Thr	Ser	Ile	Gln	Leu	Glu	Phe				



His Pro Leu Pro Ile Trp Thr Pro Ala  
695

<210> 13  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 13  
cgccagaagg gcgtgattga cgtc 24

<210> 14  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 14  
ccatccttct tcccagacag gccg 24

<210> 15  
<211> 44  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-44  
<223> Synthetic construct.

<400> 15  
gaagcctgtg tccaggtcct tcagtgagtg gtttggcctc ggtc 44

<210> 16  
<211> 1524  
<212> DNA  
<213> Homo sapiens

<400> 16  
ggcgccgcgt aggcccgagg ggccggggccg gccgggctgc gagcgctgc 50  
cccatgcgcc gcgcctctc cgcacgatgt tcccctcgcg gaggaagcg 100  
gcgcagctgc cctgggagga cggcaggtcc gggttgctct ccggcggcct 150  
ccctcggaag tgttcgctct tccacctgtt cgtggcctgc ctctcgtcg 200  
gctttctctc cctactctgg ctgcagctca gctgctctgg ggacgtggcc 250

cgggcagtca ggggacaagg gcaggagacc tcgggcccctc cccgtgcctg 300  
 ccccccagag ccgccccctg agcactggga agaagacgca tcctggggcc 350  
 cccaccgcct ggcagtgtg gtgcccttcc gcgaacgctt cgaggagctc 400  
 ctggtcttcg tgccccacat gcgccgcttc ctgagcagga agaagatccg 450  
 gcaccacatc tacgtgtcga accagggtgga ccacttcagg ttcaaccggg 500  
 cagcgctcat caacgtgggc ttcttgaga gcagcaacag cacggactac 550  
 attgccatgc acgacgttga cctgctccct ctcaacgagg agctggacta 600  
 tggctttcct gaggtgggc ccttccacgt ggctccccg gagctccacc 650  
 ctctctacca ctacaagacc tatgtoggcg gcctcctgct gctctccaag 700  
 cagcactacc ggctgtgcaa tgggatgtcc aaccgcttct ggggctgggg 750  
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 ttttccgccc ctcggaatc acaactgggt acaagacatt tcgccacctg 850  
 catgaccag cctggcgga gagggaccag aagcgcatcg cagctcaaaa 900  
 acaggagcag ttcaagggtg acaggagggg aggcctgaac actgtgaagt 950  
 accatgtggc ttcccgact gccctgtctg tgggcggggc cccctgcact 1000  
 gtcctcaaca tcatgttga ctgtgacaag accgccacac cctggtgcac 1050  
 attcagctga gctggatgga cagtgaggaa gcctgtacct acaggccata 1100  
 ttgctcaggc tcaggacaag gcctcaggtc gtgggcccag ctctgacagg 1150  
 atgtggagtg gccaggacca agacagcaag ctacgcaatt gcagccacc 1200  
 ggccgccaag gcaggcttgg gctgggcccag gacacgtggg gtgcctggga 1250  
 cgctgcttgc catgcacagt gatcagagag aggctggggg gtgtcctgtc 1300  
 cgggaccccc cctgccttcc tgetcacct actctgacct ccttcacgtg 1350  
 cccaggcctg tgggtagtgg ggagggtga acaggacaac ctctcatcac 1400  
 cctactctga cctccttcac gtgcccaggc ctgtgggtag tggggagggg 1450  
 tgaacaggac aacctctcat ccccccaaa aaaaaaaaaa aaaaaaaaaa 1500  
 aaaaaaaaaa aaaaaaaaaa aaaa 1524

<210> 17  
 <211> 327  
 <212> PRT  
 <213> Homo sapiens  
 <220>

<221> sig\_peptide  
 <222> 1-42  
 <223> Signal peptide.

<220>  
 <221> misc\_feature  
 <222> 19-25,65-71,247-253,285-291,303-310  
 <223> N-myristoylation site.

<220>  
 <221> misc\_feature  
 <222> 27-31  
 <223> cAMP- and cGMP-dependent protein kinase phosphorylation site.

<220>  
 <221> TRANSMEM  
 <222> 29-49  
 <223> Transmembrane domain (type II).

<220>  
 <221> misc\_feature  
 <222> 154-158  
 <223> N-glycosylation site.

<220>  
 <221> misc\_feature  
 <222> 226-233  
 <223> Tyrosine kinase phosphorylation site.

<400> 17  
 Met Phe Pro Ser Arg Arg Lys Ala Ala Gln Leu Pro Trp Glu Asp  
 1 5 10 15  
 Gly Arg Ser Gly Leu Leu Ser Gly Gly Leu Pro Arg Lys Cys Ser  
 20 25 30  
 Val Phe His Leu Phe Val Ala Cys Leu Ser Leu Gly Phe Phe Ser  
 35 40 45  
 Leu Leu Trp Leu Gln Leu Ser Cys Ser Gly Asp Val Ala Arg Ala  
 50 55 60  
 Val Arg Gly Gln Gly Gln Glu Thr Ser Gly Pro Pro Arg Ala Cys  
 65 70 75  
 Pro Pro Glu Pro Pro Pro Glu His Trp Glu Glu Asp Ala Ser Trp  
 80 85 90  
 Gly Pro His Arg Leu Ala Val Leu Val Pro Phe Arg Glu Arg Phe  
 95 100 105  
 Glu Glu Leu Leu Val Phe Val Pro His Met Arg Arg Phe Leu Ser  
 110 115 120  
 Arg Lys Lys Ile Arg His His Ile Tyr Val Leu Asn Gln Val Asp  
 125 130 135  
 His Phe Arg Phe Asn Arg Ala Ala Leu Ile Asn Val Gly Phe Leu



	140		145		150
Glu Ser Ser Asn Ser Thr Asp Tyr Ile	Ala Met His Asp Val Asp				
155	160				165
Leu Leu Pro Leu Asn Glu Glu Leu Asp	Tyr Gly Phe Pro Glu Ala				
170	175				180
Gly Pro Phe His Val Ala Ser Pro Glu	Leu His Pro Leu Tyr His				
185	190				195
Tyr Lys Thr Tyr Val Gly Gly Ile Leu	Leu Leu Ser Lys Gln His				
200	205				210
Tyr Arg Leu Cys Asn Gly Met Ser Asn	Arg Phe Trp Gly Trp Gly				
215	220				225
Arg Glu Asp Asp Glu Phe Tyr Arg Arg	Ile Lys Gly Ala Gly Leu				
230	235				240
Gln Leu Phe Arg Pro Ser Gly Ile Thr	Thr Gly Tyr Lys Thr Phe				
245	250				255
Arg His Leu His Asp Pro Ala Trp Arg	Lys Arg Asp Gln Lys Arg				
260	265				270
Ile Ala Ala Gln Lys Gln Glu Gln Phe	Lys Val Asp Arg Glu Gly				
275	280				285
Gly Leu Asn Thr Val Lys Tyr His Val	Ala Ser Arg Thr Ala Leu				
290	295				300
Ser Val Gly Gly Ala Pro Cys Thr Val	Leu Asn Ile Met Leu Asp				
305	310				315
Cys Asp Lys Thr Ala Thr Pro Trp Cys	Thr Phe Ser				
320	325				

<210> 18  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 18  
 gcgaacgctt cgaggagtcc tgg 23

<210> 19  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-24  
<223> Synthetic construct

<400> 19  
gcagtgcggg aagccacatg gtac 24

<210> 20  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 20  
cttcctgagc aggaagaaga tccggcacca catctacgtg ctcaac 46

<210> 21  
<211> 494  
<212> DNA  
<213> Homo sapiens

<400> 21  
caatgtttgc ctatccacct cccccaagcc cctttaccta tgctgctgct 50  
aacgctgctg ctgctgctgc tgctgcttaa aggctcatgc ttggagtggg 100  
gactggtcgg tgcccagaaa gtctcttctg ccactgacgc ccccatcagg 150  
gattgggcct tctttccccc ttcttttctg tgtctcctgc ctcatcggcc 200  
tgccatgacc tgcagccaag ccagcccccg tggggaaggg gagaaagtgg 250  
gggatggcta agaaagctgg gagatagggg acagaagagg gtagtgggtg 300  
ggctaggggg gctgccttat ttaaagtggg tgtttatgat tcttatacta 350  
atttatacaa agatattaag gccctgttca ttaagaaatt gttcccttcc 400  
cctgtgttca atgtttgtaa agattgttct gtgtaaatat gtctttataa 450  
taaacagtta aaagctgaaa aaaaaaaaaa aaaaaaaaaa aaaa 494

<210> 22  
<211> 73  
<212> PRT  
<213> Homo sapiens

<220>  
<221> sig\_peptide  
<222> 1-15  
<223> Signal peptide.

<220>  
<221> misc\_feature  
<222> 3-18

<223> Growth factor and cytokines receptors family.

<400> 22

Met Leu Leu Leu Thr Leu Leu Leu Leu Leu Leu Leu Lys Gly  
1 5 10 15  
Ser Cys Leu Glu Trp Gly Leu Val Gly Ala Gln Lys Val Ser Ser  
20 25 30  
Ala Thr Asp Ala Pro Ile Arg Asp Trp Ala Phe Phe Pro Pro Ser  
35 40 45  
Phe Leu Cys Leu Leu Pro His Arg Pro Ala Met Thr Cys Ser Gln  
50 55 60  
Ala Gln Pro Arg Gly Glu Gly Glu Lys Val Gly Asp Gly  
65 70

<210> 23

<211> 2883

<212> DNA

<213> Homo sapiens

<400> 23

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cagcggacaa aggagcatgt ccgcgcggg gaaggcccg cctccggccg 100  
ccataaggct ccggtcgccg ctgggcccgc gccgcgctcc tgcccggccg 150  
ggctccgggg cggcccgtta ggccagtgcg ccgcccgtcg cccgcagggc 200  
cccggcccgc agcatggagc caccgggacg ccggcggggc cgcgcgagc 250  
cgccgctggt gctgccgctc tcgctgttag cgctgctgc gctgctggga 300  
ggcggcggcg gcggcgggcg cgcgcgctg cccgcccggc gcaagcacga 350  
tgggcgggcc cgaggggctg gcagggcggc gggcgccgcc gagggcaagg 400  
tggtgtgcag cagcctggaa ctgcgcagg tctgcccc agatactctg 450  
cccaaccgca cggtcaccct gattctgagt aacaataaga tatccgagct 500  
gaagaatggc tcattttctg ggttaagtct ccttgaaaga ttggacctcc 550  
gaaacaatct tattagtagt atagatccag gtgccttctg gggactgtca 600  
tctctaaaaa gattggatct gacaaacaat cgaataggat gtctgaatgc 650  
agacatatat cgaggactca ccaatctggt tcggctaaac ctttcgggga 700  
atttgttttc ttattatct caaggaactt ttgattatct tgcgtcatta 750  
cggctcttgg aattccagac tgagtatctt ttgtgtgact gtaacatact 800  
gtggatgcat cgctgggtaa aggagaagaa catcacggtg cgggatacca 850

ggtgtgttta tcctaagtca ctgcaggccc aaccagtcac aggcgtgaag 900  
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 gactccatct catcgccaag ttgtgtttga aggagacagc cttcctttcc 1000  
 agtgcattggc ttcatatatt gatcaggaca tgcaagtgtt gtggtatcag 1050  
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 gaacatgatt cacaactgct ccttgattgc aagtgcccta accatttcta 1150  
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 cgtgggaata atacgaggac tgtggatatt gtggtattag agagttctgc 1250  
 acagtactgt cctccagaga ggggtggtaa caacaaaggt gacttcagat 1300  
 ggcccagAAC attggcaggc attactgcat atctgcagtg tacgcggaac 1350  
 acccatggca gtgggatata tcccggaaac ccacaggatg agagaaaagc 1400  
 ttggcgcaga tgtgatagag gtggcttttg ggcagatgat gattattctc 1450  
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 ttacactgtg gaagcagcca acttttctga caaatggat gttatatttg 1600  
 tggcagaaat gattgaaaaa tttggaagat ttaccaagga ggaaaaatca 1650  
 aaagagctag gtgacgtgat ggttgacatt gcaagtaaca tcatgttggc 1700  
 tgatgaacgt gtccctgtggc tggcgcagag ggaagctaaa gcctgcagta 1750  
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 gctcacgttt attcaacata ttcaoccaa attgctctgg aagcttatgt 1850  
 catcaagtct actggcttca cggggatgac ctgtaccgtg ttccagaaag 1900  
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 gagggaaacc tggataagca gctgagcttt aagtgcaatg tttcaaatac 2000  
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acatgtgaaa aaatatttatt tgacttaaaa gtttatttat ttgttttttt 2350  
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 agaccaggtg tttaatcaag caagctgtat atcaaaattt ttggcagaaa 2500  
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<210> 24  
 <211> 616  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-33  
 <223> Signal peptide.

<220>  
 <221> TRANSMEM  
 <222> 13-40  
 <223> Transmembrane domain (type II).

<400> 24  
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 Leu Leu Pro Leu Ser Leu Leu Ala Leu Leu Ala Leu Leu Gly Gly  
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 Gly Gly Gly Gly Gly Ala Ala Ala Leu Pro Ala Gly Cys Lys His  
 35 40 45  
 Asp Gly Arg Pro Arg Gly Ala Gly Arg Ala Ala Gly Ala Ala Glu  
 50 55 60  
 Gly Lys Val Val Cys Ser Ser Leu Glu Leu Ala Gln Val Leu Pro  
 65 70 75  
 Pro Asp Thr Leu Pro Asn Arg Thr Val Thr Leu Ile Leu Ser Asn  
 80 85 90

Asn Lys Ile Ser	Glu 95	Leu Lys Asn Gly	Ser 100	Phe Ser Gly	Leu 105
Leu Leu Glu Arg	Leu 110	Asp Leu Arg Asn	Asn 115	Leu Ile Ser	Ser 120
Asp Pro Gly Ala	Phe 125	Trp Gly Leu Ser	Ser 130	Leu Lys Arg	Leu 135
Leu Thr Asn Asn	Arg 140	Ile Gly Cys Leu	Asn 145	Ala Asp Ile	Phe 150
Gly Leu Thr Asn	Leu 155	Val Arg Leu Asn	Leu 160	Ser Gly Asn	Leu 165
Ser Ser Leu Ser	Gln 170	Gly Thr Phe Asp	Tyr 175	Leu Ala Ser	Leu 180
Ser Leu Glu Phe	Gln 185	Thr Glu Tyr Leu	Leu 190	Cys Asp Cys	Asn 195
Leu Trp Met His	Arg 200	Trp Val Lys Glu	Lys 205	Asn Ile Thr	Val 210
Asp Thr Arg Cys	Val 215	Tyr Pro Lys Ser	Leu 220	Gln Ala Gln	Pro 225
Thr Gly Val Lys	Gln 230	Glu Leu Leu Thr	Cys 235	Asp Pro Pro	Leu 240
Leu Pro Ser Phe	Tyr 245	Met Thr Pro Ser	His 250	Arg Gln Val	Val 255
Glu Gly Asp Ser	Leu 260	Pro Phe Gln Cys	Met 265	Ala Ser Tyr	Ile 270
Gln Asp Met Gln	Val 275	Leu Trp Tyr Gln	Asp 280	Gly Arg Ile	Val 285
Thr Asp Glu Ser	Gln 290	Gly Ile Phe Val	Glu 295	Lys Asn Met	Ile 300
Asn Cys Ser Leu	Ile 305	Ala Ser Ala Leu	Thr 310	Ile Ser Asn	Ile 315
Ala Gly Ser Thr	Gly 320	Asn Trp Gly Cys	His 325	Val Gln Thr	Lys 330
Gly Asn Asn Thr	Arg 335	Thr Val Asp Ile	Val 340	Val Leu Glu	Ser 345
Ala Gln Tyr Cys	Pro 350	Pro Glu Arg Val	Val 355	Asn Asn Lys	Gly 360
Phe Arg Trp Pro	Arg 365	Thr Leu Ala Gly	Ile 370	Thr Ala Tyr	Leu 375
Cys Thr Arg Asn	Thr	His Gly Ser Gly	Ile	Tyr Pro Gly	Asn Pro

	380		385		390
Gln Asp Glu Arg	Lys Ala Trp Arg Arg	Cys Asp Arg Gly Gly	Phe		
	395	400	405		
Trp Ala Asp Asp	Asp Tyr Ser Arg Cys	Gln Tyr Ala Asn Asp	Val		
	410	415	420		
Thr Arg Val Leu	Tyr Met Phe Asn Gln	Met Pro Leu Asn Leu	Thr		
	425	430	435		
Asn Ala Val Ala	Thr Ala Arg Gln Leu	Leu Ala Tyr Thr Val	Glu		
	440	445	450		
Ala Ala Asn Phe	Ser Asp Lys Met Asp	Val Ile Phe Val Ala	Glu		
	455	460	465		
Met Ile Glu Lys	Phe Gly Arg Phe Thr	Lys Glu Glu Lys Ser	Lys		
	470	475	480		
Glu Leu Gly Asp	Val Met Val Asp Ile	Ala Ser Asn Ile Met	Leu		
	485	490	495		
Ala Asp Glu Arg	Val Leu Trp Leu Ala	Gln Arg Glu Ala Lys	Ala		
	500	505	510		
Cys Ser Arg Ile	Val Gln Cys Leu Gln	Arg Ile Ala Thr Tyr	Arg		
	515	520	525		
Leu Ala Gly Gly	Ala His Val Tyr Ser	Thr Tyr Ser Pro Asn	Ile		
	530	535	540		
Ala Leu Glu Ala	Tyr Val Ile Lys Ser	Thr Gly Phe Thr Gly	Met		
	545	550	555		
Thr Cys Thr Val	Phe Gln Lys Val Ala	Ala Ser Asp Arg Thr	Gly		
	560	565	570		
Leu Ser Asp Tyr	Gly Arg Arg Asp Pro	Glu Gly Asn Leu Asp	Lys		
	575	580	585		
Gln Leu Ser Phe	Lys Cys Asn Val Ser	Asn Thr Phe Ser Ser	Leu		
	590	595	600		
Ala Leu Lys Val	Cys Tyr Ile Leu Gln	Ser Phe Lys Thr Ile	Tyr		
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Ser

<210> 25  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24

<223> Synthetic construct

<400> 25

gaggactcac caatctgggtt cggc 24

<210> 26

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 26

aactggaaaag gaaggctgtc tccc 24

<210> 27

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 27

gtaaaggaga agaacatcac ggtacgggat accagggtgtg tttatcctaa 50

<210> 28

<211> 683

<212> DNA

<213> Homo sapiens

<400> 28

gcgtggggat gtctaggagc tcgaagggtg tgctgggcct ctcggtgctg 50

ctgacggcgg ccacagtggc cggcgtacat gtgaagcagc agtgggacca 100

gcagaggctt cgtgacggag ttatcagaga cattgagagg caaattcgga 150

aaaaagaaaa cattcgtctt ttggggagaac agattatctt gactgagcaa 200

cttgaagcag aaagagagaa gatgttattg gcaaaaaggat ctcaaaaatc 250

atgacttgaa tgtgaaatat ctgttggaca gacaacacga gtttgtgtgt 300

gtgtgttgat ggagagtagc ttagtagtat cttcatcttt ttttttggtc 350

actgtccttt taaacttgat caaataaagg acagtgggtc atataagtta 400

ctgctttcag ggtcccttat atctgaataa aggagtgtgg gcagacactt 450

tttggaaagag tctgtctggg tgatcctggt agaagcccca ttagggtcac 500

tgtccagtgc ttagggttgt tactgagaag cactgccgag cttgtgagaa 550



ggaagggatg gatagtagca tccacctgag tagtctgatc agtcggcatg 600  
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 gtggagggag agacgctcct gatcgtcgaa tcc 683

<210> 29  
 <211> 81  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> sig\_peptide  
 <222> 1-21  
 <223> Signal peptide.

<400> 29  
 Met Ser Arg Ser Ser Lys Val Val Leu Gly Leu Ser Val Leu Leu  
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 Thr Ala Ala Thr Val Ala Gly Val His Val Lys Gln Gln Trp Asp  
                   20                  25                  30  
 Gln Gln Arg Leu Arg Asp Gly Val Ile Arg Asp Ile Glu Arg Gln  
                   35                  40                  45  
 Ile Arg Lys Lys Glu Asn Ile Arg Leu Leu Gly Glu Gln Ile Ile  
                   50                  55                  60  
 Leu Thr Glu Gln Leu Glu Ala Glu Arg Glu Lys Met Leu Leu Ala  
                   65                  70                  75  
 Lys Gly Ser Gln Lys Ser  
                   80

<210> 30  
 <211> 2128  
 <212> DNA  
 <213> Homo sapiens

<400> 30  
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 tacagcctgt tccaagtgtg gcttaatcgg tctccaccac cagatctttc 100  
 tccgtggatt cctctgctaa gaccgctgcc atgccagtga cggtaaccgg 150  
 caccaccatc acaaccacca cgacgtcatc ttcgggcctg gggcccccca 200  
 tgatcgtggg gtccccctgg gccctgacac agcccctggg tctccttcgc 250  
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 gggcgcctgg acgggggtcca tgggcaactg gtccatgttc acctggtgct 350  
 tctgcttctc cgtgaccctg atcatcctca tcgtggagct gtgcgggctc 400  
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ctatgcggcc ctctttctgcc tctcggcctc catcatctac cccaccacct 500  
atgtccagtt cctgtcccaac ggccgttcgc gggaccacgc catcgccgcc 550  
accttcttct cctgcacgc gtgtgtggct tacgccaccg aagtggcctg 600  
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ctggcccctc taccagttcg atgagaagta tggcggccag cctcggcgct 950  
cgagagatgt aagctgcagc cgcagccatg cctactacgt gtgtgcctgg 1000  
gaccgccgac tggtgtggc catcctgacg gccatcaacc tactggcgta 1050  
tgtggctgac ctggtgcact ctgccacct ggtttttgtc aaggtctaag 1100  
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<210> 31  
 <211> 322  
 <212> PRT  
 <213> Homo sapiens

<400> 31  
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 35 40 45  
 Ser Thr Cys Val Ala Phe Ser Leu Val Ala Ser Val Gly Ala Trp  
 50 55 60  
 Thr Gly Ser Met Gly Asn Trp Ser Met Phe Thr Trp Cys Phe Cys  
 65 70 75  
 Phe Ser Val Thr Leu Ile Ile Leu Ile Val Glu Leu Cys Gly Leu  
 80 85 90  
 Gln Ala Arg Phe Pro Leu Ser Trp Arg Asn Phe Pro Ile Thr Phe  
 95 100 105  
 Ala Cys Tyr Ala Ala Leu Phe Cys Leu Ser Ala Ser Ile Ile Tyr  
 110 115 120  
 Pro Thr Thr Tyr Val Gln Phe Leu Ser His Gly Arg Ser Arg Asp  
 125 130 135  
 His Ala Ile Ala Ala Thr Phe Phe Ser Cys Ile Ala Cys Val Ala  
 140 145 150  
 Tyr Ala Thr Glu Val Ala Trp Thr Arg Ala Arg Pro Gly Glu Ile  
 155 160 165  
 Thr Gly Tyr Met Ala Thr Val Pro Gly Leu Leu Lys Val Leu Glu  
 170 175 180  
 Thr Phe Val Ala Cys Ile Ile Phe Ala Phe Ile Ser Asp Pro Asn  
 185 190 195  
 Leu Tyr Gln His Gln Pro Ala Leu Glu Trp Cys Val Ala Val Tyr  
 200 205 210

Ala Ile Cys Phe Ile Leu Ala Ala Ile Ala Ile Leu Leu Asn Leu  
215 220 225

Gly Glu Cys Thr Asn Val Leu Pro Ile Pro Phe Pro Ser Phe Leu  
230 235 240

Ser Gly Leu Ala Leu Leu Ser Val Leu Leu Tyr Ala Thr Ala Leu  
245 250 255

Val Leu Trp Pro Leu Tyr Gln Phe Asp Glu Lys Tyr Gly Gly Gln  
260 265 270

Pro Arg Arg Ser Arg Asp Val Ser Cys Ser Arg Ser His Ala Tyr  
275 280 285

Tyr Val Cys Ala Trp Asp Arg Arg Leu Ala Val Ala Ile Leu Thr  
290 295 300

Ala Ile Asn Leu Leu Ala Tyr Val Ala Asp Leu Val His Ser Ala  
305 310 315

His Leu Val Phe Val Lys Val  
320

<210> 32  
<211> 3680  
<212> DNA  
<213> Homo sapiens

<400> 32  
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taatataaaa atctttgtaa atctctaaaa 3680

<210> 33

<211> 335

<212> PRT

<213> Homo sapiens

<400> 33

Met	Phe	Leu	Ala	Thr	Leu	Ser	Phe	Leu	Leu	Pro	Phe	Ala	His	Pro
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Phe	Gly	Thr	Val	Ser	Cys	Glu	Tyr	Met	Leu	Gly	Ser	Pro	Leu	Ser
				20					25					30

Ser	Leu	Ala	Gln	Val	Asn	Leu	Ser	Pro	Phe	Ser	His	Pro	Lys	Val
				35					40					45

His	Met	Asp	Pro	Asn	Tyr	Cys	His	Pro	Ser	Thr	Ser	Leu	His	Leu
				50					55					60

Cys	Ser	Leu	Ala	Trp	Ser	Phe	Thr	Arg	Leu	Leu	His	Pro	Pro	Leu
				65					70					75

Ser	Pro	Gly	Ile	Ser	Gln	Val	Val	Lys	Asp	His	Val	Thr	Lys	Pro
				80					85					90

Thr	Ala	Met	Ala	Gln	Gly	Arg	Val	Ala	His	Leu	Ile	Glu	Trp	Lys
				95					100					105

Gly	Trp	Ser	Lys	Pro	Ser	Asp	Ser	Pro	Ala	Ala	Leu	Glu	Ser	Ala
				110					115					120

Phe	Ser	Ser	Tyr	Ser	Asp	Leu	Ser	Glu	Gly	Glu	Gln	Glu	Ala	Arg
				125					130					135

Phe	Ala	Ala	Gly	Val	Ala	Glu	Gln	Phe	Ala	Ile	Ala	Glu	Ala	Lys
				140					145					150

Leu	Arg	Ala	Trp	Ser	Ser	Val	Asp	Gly	Glu	Asp	Ser	Thr	Asp	Asp
				155					160					165

Ser	Tyr	Asp	Glu	Asp	Phe	Ala	Gly	Gly	Met	Asp	Thr	Asp	Met	Ala
				170					175					180

Gly	Gln	Leu	Pro	Leu	Gly	Pro	His	Leu	Gln	Asp	Leu	Phe	Thr	Gly
				185					190					195

His	Arg	Phe	Ser	Arg	Pro	Val	Arg	Gln	Gly	Ser	Val	Glu	Pro	Glu
				200					205					210

Ser	Asp	Cys	Ser	Gln	Thr	Val	Ser	Pro	Asp	Thr	Leu	Cys	Ser	Ser
				215					220					225

Leu	Cys	Ser	Leu	Glu	Asp	Gly	Leu	Leu	Gly	Ser	Pro	Ala	Arg	Leu
				230					235					240

Ala Ser Gln Leu Leu Gly Asp Glu Leu Leu Leu Ala Lys Leu Pro  
245 250 255

Pro Ser Arg Glu Ser Ala Phe Arg Ser Leu Gly Pro Leu Glu Ala  
260 265 270

Gln Asp Ser Leu Tyr Asn Ser Pro Leu Thr Glu Ser Cys Leu Ser  
275 280 285

Pro Ala Glu Glu Glu Pro Ala Pro Cys Lys Asp Cys Gln Pro Leu  
290 295 300

Cys Pro Pro Leu Thr Gly Ser Trp Glu Arg Gln Arg Gln Ala Ser  
305 310 315

Asp Leu Ala Ser Ser Gly Val Val Ser Leu Asp Glu Asp Glu Ala  
320 325 330

Glu Pro Glu Glu Gln  
335

<210> 34  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct

<400> 34  
tgtcctttgt ccagacttc tgtcc 25

<210> 35  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 35  
ctggatgcta atgtgtccag taaatgatcc ccttatcccg tcgcatgct 50

<210> 36  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 36



ttccactcaa tgaggtgagc cactc 25

<210> 37  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 37  
 ggcgagccct aactatccag gag 23

<210> 38  
 <211> 39  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-39  
 <223> Synthetic construct.

<400> 38  
 ggagatcgct gcgctggcca ggtcctccct gcatggat 39

<210> 39  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 39  
 ctgctgcaaa gcgagcctct tg 22

<210> 40  
 <211> 2084  
 <212> DNA  
 <213> Homo sapiens

<400> 40  
 ggttcctggg cgctctgtta cacaagcaag atacagccag cccaccta 50  
 ttttgtttcc ctggcaccct cctgctcagt ggcacattgt cacacttaac 100  
 ccatctgttt tctctaattgc acgacagatt cctttcagac aggacaactg 150  
 tgatatttca gttcctgatt gtaaatacct cctaagcctg aagcttctgt 200  
 tactagccat tgtgagcttc agttttcttca tctgcaaaat gggcataata 250  
 caatctattc ttgccacatc aagggttctg tattccttta aaaaaaac 300



attgaaaggg tgcttttttaa agaaaatttg acttaaagct aaaaagagga 1800  
catagcccag agtttctggtt attgggaaat tgaggcaata gaaatgacag 1850  
acctgtattc tagtacgtta taattttcta gatcagcaca cacatgatca 1900  
gccactgag ttatgaagct gacaatgact gcattcaacg gggccatggc 1950  
aggaaagctg accctacca ggaaagtaat agcttcttta aaagtcttca 2000  
aaggttttgg gaattttaac ttgtcttaat atatcttagg cttcaattat 2050  
ttgggtgcoct taaaaactca atgagaatca tgggt 2084

<210> 41  
<211> 334  
<212> PRT  
<213> Homo sapiens

<400> 41  
Met Leu Ala Leu Ala Lys Ile Leu Leu Ile Ser Thr Leu Phe Tyr  
1 5 10 15  
Ser Leu Leu Ser Gly Ser His Gly Lys Glu Asn Gln Asp Ile Asn  
20 25 30  
Thr Thr Gln Asn Ile Ala Glu Val Phe Lys Thr Met Glu Asn Lys  
35 40 45  
Pro Ile Ser Leu Glu Ser Glu Ala Asn Leu Asn Ser Asp Lys Glu  
50 55 60  
Asn Ile Thr Thr Ser Asn Leu Lys Ala Ser His Ser Pro Pro Leu  
65 70 75  
Asn Leu Pro Asn Asn Ser His Gly Ile Thr Asp Phe Ser Ser Asn  
80 85 90  
Ser Ser Ala Glu His Ser Leu Gly Ser Leu Lys Pro Thr Ser Thr  
95 100 105  
Ile Ser Thr Ser Pro Pro Leu Ile His Ser Phe Val Ser Lys Val  
110 115 120  
Pro Trp Asn Ala Pro Ile Ala Asp Glu Asp Leu Leu Pro Ile Ser  
125 130 135  
Ala His Pro Asn Ala Thr Pro Ala Leu Ser Ser Glu Asn Phe Thr  
140 145 150  
Trp Ser Leu Val Asn Asp Thr Val Lys Thr Pro Asp Asn Ser Ser  
155 160 165  
Ile Thr Val Ser Ile Leu Ser Ser Glu Pro Thr Ser Pro Ser Val  
170 175 180  
Thr Pro Leu Ile Val Glu Pro Ser Gly Trp Leu Thr Thr Asn Ser  
185 190 195

Asp	Ser	Phe	Thr	Gly	Phe	Thr	Pro	Tyr	Gln	Glu	Lys	Thr	Thr	Leu
				200					205					210
Gln	Pro	Thr	Leu	Lys	Phe	Thr	Asn	Asn	Ser	Lys	Leu	Phe	Pro	Asn
				215					220					225
Thr	Ser	Asp	Pro	Gln	Lys	Glu	Asn	Arg	Asn	Thr	Gly	Ile	Val	Phe
				230					235					240
Gly	Ala	Ile	Leu	Gly	Ala	Ile	Leu	Gly	Val	Ser	Leu	Leu	Thr	Leu
				245					250					255
Val	Gly	Tyr	Leu	Leu	Cys	Gly	Lys	Arg	Lys	Thr	Asp	Ser	Phe	Ser
				260					265					270
His	Arg	Arg	Leu	Tyr	Asp	Asp	Arg	Asn	Glu	Pro	Val	Leu	Arg	Leu
				275					280					285
Asp	Asn	Ala	Pro	Glu	Pro	Tyr	Asp	Val	Ser	Phe	Gly	Asn	Ser	Ser
				290					295					300
Tyr	Tyr	Asn	Pro	Thr	Leu	Asn	Asp	Ser	Ala	Met	Pro	Glu	Ser	Glu
				305					310					315
Glu	Asn	Ala	Arg	Asp	Gly	Ile	Pro	Met	Asp	Asp	Ile	Pro	Pro	Leu
				320					325					330

Arg Thr Ser Val

<210> 42  
 <211> 1594  
 <212> DNA  
 <213> Homo sapiens

<400> 42  
 aacaggatct cctcttgcag tctgcagccc aggacgctga ttccagcagc 50  
 gccttaccgc gcagcccgaa gattcactat ggtgaaaatc gccttcaata 100  
 cccctaccgc cgtgcaaaaag gaggaggcgc ggcaagacgt ggaggccctc 150  
 ctgagccgca cggtcagaac tcagatactg accggcaagg agctccgagt 200  
 tgccaccag gaaaaagagg gctcctctgg gagatgtatg cttactctct 250  
 taggcctttc attcatcttg gcaggactta ttgttggtgg agcctgcatt 300  
 tacaagtact tcatgcccga gagcaccatt taccgtggag agatgtgctt 350  
 ttttgattct gaggatcctg caaattccct tcgtggagga gagcctaact 400  
 tcctgcctgt gactgaggag gctgacattc gtgaggatga caacattgca 450  
 atcattgatg tgcctgtccc cagtttctct gatagtgacc ctgcagcaat 500  
 tattcatgac ttgaaaaagg gaatgactgc ttacctggac ttgttgctgg 550



50										55					60				
Ser	Phe	Ile	Leu	Ala	Gly	Leu	Ile	Val	Gly	Gly	Ala	Cys	Ile	Tyr					
				65					70					75					
Lys	Tyr	Phe	Met	Pro	Lys	Ser	Thr	Ile	Tyr	Arg	Gly	Glu	Met	Cys					
				80					85					90					
Phe	Phe	Asp	Ser	Glu	Asp	Pro	Ala	Asn	Ser	Leu	Arg	Gly	Gly	Glu					
				95					100					105					
Pro	Asn	Phe	Leu	Pro	Val	Thr	Glu	Glu	Ala	Asp	Ile	Arg	Glu	Asp					
				110					115					120					
Asp	Asn	Ile	Ala	Ile	Ile	Asp	Val	Pro	Val	Pro	Ser	Phe	Ser	Asp					
				125					130					135					
Ser	Asp	Pro	Ala	Ala	Ile	Ile	His	Asp	Phe	Glu	Lys	Gly	Met	Thr					
				140					145					150					
Ala	Tyr	Leu	Asp	Leu	Leu	Leu	Gly	Asn	Cys	Tyr	Leu	Met	Pro	Leu					
				155					160					165					
Asn	Thr	Ser	Ile	Val	Met	Pro	Pro	Lys	Asn	Leu	Val	Glu	Leu	Phe					
				170					175					180					
Gly	Lys	Leu	Ala	Ser	Gly	Arg	Tyr	Leu	Pro	Gln	Thr	Tyr	Val	Val					
				185					190					195					
Arg	Glu	Asp	Leu	Val	Ala	Val	Glu	Glu	Ile	Arg	Asp	Val	Ser	Asn					
				200					205					210					
Leu	Gly	Ile	Phe	Ile	Tyr	Gln	Leu	Cys	Asn	Asn	Arg	Lys	Ser	Phe					
				215					220					225					
Arg	Leu	Arg	Arg	Arg	Asp	Leu	Leu	Leu	Gly	Phe	Asn	Lys	Arg	Ala					
				230					235					240					
Ile	Asp	Lys	Cys	Trp	Lys	Ile	Arg	His	Phe	Pro	Asn	Glu	Phe	Ile					
				245					250					255					
Val	Glu	Thr	Lys	Ile	Cys	Gln	Glu												
				260															

<210> 44

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-24

<223> Synthetic construct.

<400> 44

gaaagacacg acacagcagc ttgc 24

<210> 45

<211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 45  
 gggaactgct atctgatgcc 20

<210> 46  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 46  
 caggatctcc tcttgcatgc tgcagc 26

<210> 47  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 47  
 cttctcgaac cacataagtt tgaggcag 28

<210> 48  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 48  
 cacgattccc tccacagcaa ctggg 25

<210> 49  
 <211> 1969  
 <212> DNA  
 <213> Homo sapiens

<400> 49  
 ggaggagggga gggcgggcag gcgccagccc agagcagccc cgggcaccag 50

cacggactct ctcttccagc ccagggtgcc cccactctcg ctccattcgg 100  
cgggagcacc cagtcctgta cgccaaggaa ctggtcctgg gggcaccatg 150  
gtttcggcgg cagccccag cctcctcatc cttctgttgc tgctgctggg 200  
gtctgtgcct gctaccgacg cccgctctgt gccctgaag gccacgttcc 250  
tggaggatgt ggcgggtagt ggggaggccg agggctcgtc ggcctcctcc 300  
ccgagcctcc cgccaccctg gaccccggcc ctacagccca catcgatggg 350  
gccccagccc acaaccctgg ggggcccata acccccacc aacttcctgg 400  
atgggatagt ggacttcttc cgccagtacg tgatgctgat tgctgtggtg 450  
ggctccctgg cctttctgct gatgttcata gtctgtgccg cggtcatac 500  
ccggcagaag cagaaggcct cggcctatta cccatcgtcc ttccccaaga 550  
agaagtacgt ggaccagagt gaccgggccc ggggcccccg ggccttcagt 600  
gagggtcccc acagagcccc cgacagcagg cccgaggaag ccctggattc 650  
ctcccggcag ctccaggccg acatcttggc cgccaccag aacctcaagt 700  
ccccaccag ggctgcactg ggcggtgggg acggagccag gatggtggag 750  
ggcaggggcg cagaggaaga ggagaagggc agccaggagg gggaccagga 800  
agtccaggga catgggggtcc cagtggagac accagaggcg caggaggagc 850  
cgtgctcagg ggtccttgag ggggctgtgg tggccggtga gggccaaggg 900  
gagctggaag ggtctctctt gttagcccag gaagcccagg gaccagtggg 950  
tcccccgaa agcccctgtg cttgcagcag tgtccacccc agtgtctaac 1000  
agtcctcccg ggctgccagc cctgactgtc gggcccccaa gtggtcacct 1050  
ccccgtgtat gaaaaggcct tcagccctga ctgcttctg aactccctc 1100  
cttggcctcc ctgtggtgcc aatcccagca tgtgctgatt ctacagcagg 1150  
cagaaatgct ggtccccggt gcccggagg aatcttacca agtgccatca 1200  
tccttcacct cagcagcccc aaagggtac atcctacagc acagctcccc 1250  
tgacaaaagt agggagggca cgtgtccctg tgacagccag gataaaacat 1300  
ccccaaagt gctgggatta caggcgtgag ccaccgtgcc cggccaaac 1350  
tactttttaa aacagctaca gggtaaaatc ctgcagcacc cactctggaa 1400  
aatactgctc ttaattttcc tgaagggtgg cccctgttct tagttggtcc 1450  
aggattaggg atgtggggta tagggcattt aaatcctctc aagcgtctc 1500



caagcacccc cggcctgggg gtgagtttct catcccgcta ctgctgctgg 1550  
 gatcagggttg aatgaatgga actcttcctg tctggcctcc aaagcagcct 1600  
 agaagctgag gggctgtggt tgagggggacc tccaccctgg ggaagtccga 1650  
 ggggctgggg aagggttttct gacgcccagc ctggagcagg ggggccctgg 1700  
 ccaccccctg ttgctcacac attgtctggc agcctgtgtc cacaatattc 1750  
 gtcagtcctc gacagggagc ctgggctccg tctgcttta gggaggctct 1800  
 ggcaggaggt cctctcccc atccctccat ctggggctcc cccaacctct 1850  
 gcacagctct ccagggtgtg agatataatg caccagcaca ataaaccttt 1900  
 attccggcct gaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1950  
 aaaaaaaaaa aaaaaaaga 1969

<210> 50  
 <211> 283  
 <212> PRT  
 <213> Homo sapiens

<400> 50  
 Met Val Ser Ala Ala Ala Pro Ser Leu Leu Ile Leu Leu Leu Leu  
 1 5 10 15  
 Leu Leu Gly Ser Val Pro Ala Thr Asp Ala Arg Ser Val Pro Leu  
 20 25 30  
 Lys Ala Thr Phe Leu Glu Asp Val Ala Gly Ser Gly Glu Ala Glu  
 35 40 45  
 Gly Ser Ser Ala Ser Ser Pro Ser Leu Pro Pro Pro Trp Thr Pro  
 50 55 60  
 Ala Leu Ser Pro Thr Ser Met Gly Pro Gln Pro Thr Thr Leu Gly  
 65 70 75  
 Gly Pro Ser Pro Pro Thr Asn Phe Leu Asp Gly Ile Val Asp Phe  
 80 85 90  
 Phe Arg Gln Tyr Val Met Leu Ile Ala Val Val Gly Ser Leu Ala  
 95 100 105  
 Phe Leu Leu Met Phe Ile Val Cys Ala Ala Val Ile Thr Arg Gln  
 110 115 120  
 Lys Gln Lys Ala Ser Ala Tyr Tyr Pro Ser Ser Phe Pro Lys Lys  
 125 130 135  
 Lys Tyr Val Asp Gln Ser Asp Arg Ala Gly Gly Pro Arg Ala Phe  
 140 145 150  
 Ser Glu Val Pro Asp Arg Ala Pro Asp Ser Arg Pro Glu Glu Ala  
 155 160 165

Leu	Asp	Ser	Ser	Arg	Gln	Leu	Gln	Ala	Asp	Ile	Leu	Ala	Ala	Thr	
				170					175					180	
Gln	Asn	Leu	Lys	Ser	Pro	Thr	Arg	Ala	Ala	Leu	Gly	Gly	Gly	Asp	
				185					190					195	
Gly	Ala	Arg	Met	Val	Glu	Gly	Arg	Gly	Ala	Glu	Glu	Glu	Glu	Lys	
				200					205					210	
Gly	Ser	Gln	Glu	Gly	Asp	Gln	Glu	Val	Gln	Gly	His	Gly	Val	Pro	
				215					220					225	
Val	Glu	Thr	Pro	Glu	Ala	Gln	Glu	Glu	Pro	Cys	Ser	Gly	Val	Leu	
				230					235					240	
Glu	Gly	Ala	Val	Val	Ala	Gly	Glu	Gly	Gln	Gly	Glu	Leu	Glu	Gly	
				245					250					255	
Ser	Leu	Leu	Leu	Ala	Gln	Glu	Ala	Gln	Gly	Pro	Val	Gly	Pro	Pro	
				260					265					270	
Glu	Ser	Pro	Cys	Ala	Cys	Ser	Ser	Val	His	Pro	Ser	Val			
				275					280						

<210> 51  
 <211> 1734  
 <212> DNA  
 <213> Homo sapiens

<400> 51  
 gtggactctg agaagcccag gcagttgagg acaggagaga gaaggctgca 50  
 gaccagagg gagggaggac agggagtcgg aaggaggagg acagaggagg 100  
 gcacagagac gcagagcaag ggcggcaagg aggagaccct ggtgggagga 150  
 agacactctg gagagagagg gggctgggca gagatgaagt tccaggggcc 200  
 cctggcctgc ctctgctgg ccctctgcct gggcagtggg gaggctggcc 250  
 ccctgcagag cggagaggaa agcactggga caaatattgg ggaggccctt 300  
 ggacatggcc tgggagacgc cctgagcgaa ggggtgggaa aggccattgg 350  
 caaagaggcc ggaggggcag ctggctctaa agtcagttag gcccttggcc 400  
 aagggaccag agaagcagtt ggcactggag tcaggcaggt tccaggcttt 450  
 ggcgcagcag atgctttggg caacagggtc ggggaagcag cccatgctct 500  
 gggaaacact gggcacgaga ttggcagaca ggcagaagat gtcattcgac 550  
 acggagcaga tgctgtccgc ggctcctggc agggggtgcc tggccacagt 600  
 ggtgcttggg aaacttctgg aggccatggc atctttggct ctcaaggtgg 650  
 ccttggaggc cagggccagg gcaatcctgg aggtctgggg actccgtggg 700

tccacggata ccccggaac tcagcaggca gctttggaat gaatcctcag 750  
 ggagctccct ggggtcaagg aggcaatgga gggccaccaa actttgggac 800  
 caaactcag ggagctgtgg ccagcctgg ctatggttca gtgagagcca 850  
 gcaaccagaa tgaagggtgc acgaatcccc caccatctgg ctcaggtgga 900  
 ggctccagca actctggggg aggcagcggc tcacagtcgg gcagcagtgg 950  
 cagtggcagc aatggtgaca acaacaatgg cagcagcagt ggtggcagca 1000  
 gcagtggcag cagcagtggc agcagcagtg gcggcagcag tggcggcagc 1050  
 agtgggtggca gcagtggcaa cagtgggtggc agcagaggtg acagcggcag 1100  
 tgagtctctc tggggatcca gcaccggctc ctctccggc aaccacggtg 1150  
 ggagcggcgg aggaaatgga cataaaccg ggtgtgaaaa gccagggaat 1200  
 gaagcccgcg ggagcgggga atctgggatt cagggttca gaggacaggg 1250  
 agtttccagc aacatgaggg aaataagcaa agagggcaat cgcctccttg 1300  
 gaggtcttg agacaattat cgggggcaag ggtcgagctg gggcagtgga 1350  
 ggaggtgacg ctgttggtgg agtcaatact gtgaactctg agacgtctcc 1400  
 tgggatgttt aactttgaca ctttctggaa gaattttaaa tccaagctgg 1450  
 gtttcatcaa ctgggatgcc ataaacaagg accagagaag ctctcgcac 1500  
 ccgtgacctc cagacaagga gccaccagat tggatgggag cccccacact 1550  
 ccctccttaa aacaccaccc tctcatcact aatctcagcc cttgcccttg 1600  
 aaataaacct tagctgcccc aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1734

<210> 52  
 <211> 440  
 <212> PRT  
 <213> Homo sapiens

<400> 52  
 Met Lys Phe Gln Gly Pro Leu Ala Cys Leu Leu Leu Ala Leu Cys  
 1 5 10 15  
 Leu Gly Ser Gly Glu Ala Gly Pro Leu Gln Ser Gly Glu Glu Ser  
 20 25 30  
 Thr Gly Thr Asn Ile Gly Glu Ala Leu Gly His Gly Leu Gly Asp  
 35 40 45  
 Ala Leu Ser Glu Gly Val Gly Lys Ala Ile Gly Lys Glu Ala Gly

	50		55		60
Gly Ala Ala Gly Ser Lys Val Ser Glu Ala Leu Gly Gln Gly Thr	65		70		75
Arg Glu Ala Val Gly Thr Gly Val Arg Gln Val Pro Gly Phe Gly	80		85		90
Ala Ala Asp Ala Leu Gly Asn Arg Val Gly Glu Ala Ala His Ala	95		100		105
Leu Gly Asn Thr Gly His Glu Ile Gly Arg Gln Ala Glu Asp Val	110		115		120
Ile Arg His Gly Ala Asp Ala Val Arg Gly Ser Trp Gln Gly Val	125		130		135
Pro Gly His Ser Gly Ala Trp Glu Thr Ser Gly Gly His Gly Ile	140		145		150
Phe Gly Ser Gln Gly Gly Leu Gly Gly Gln Gly Gln Gly Asn Pro	155		160		165
Gly Gly Leu Gly Thr Pro Trp Val His Gly Tyr Pro Gly Asn Ser	170		175		180
Ala Gly Ser Phe Gly Met Asn Pro Gln Gly Ala Pro Trp Gly Gln	185		190		195
Gly Gly Asn Gly Gly Pro Pro Asn Phe Gly Thr Asn Thr Gln Gly	200		205		210
Ala Val Ala Gln Pro Gly Tyr Gly Ser Val Arg Ala Ser Asn Gln	215		220		225
Asn Glu Gly Cys Thr Asn Pro Pro Pro Ser Gly Ser Gly Gly Gly	230		235		240
Ser Ser Asn Ser Gly Gly Gly Ser Gly Ser Gln Ser Gly Ser Ser	245		250		255
Gly Ser Gly Ser Asn Gly Asp Asn Asn Asn Gly Ser Ser Ser Gly	260		265		270
Gly Ser Ser Ser Gly Ser Ser Ser Gly Ser Ser Ser Gly Gly Ser	275		280		285
Ser Gly Gly Ser Ser Gly Gly Ser Ser Gly Asn Ser Gly Gly Ser	290		295		300
Arg Gly Asp Ser Gly Ser Glu Ser Ser Trp Gly Ser Ser Thr Gly	305		310		315
Ser Ser Ser Gly Asn His Gly Gly Ser Gly Gly Gly Asn Gly His	320		325		330
Lys Pro Gly Cys Glu Lys Pro Gly Asn Glu Ala Arg Gly Ser Gly	335		340		345

Glu Ser Gly Ile Gln Gly Phe Arg Gly Gln Gly Val Ser Ser Asn  
 350 355 360  
 Met Arg Glu Ile Ser Lys Glu Gly Asn Arg Leu Leu Gly Gly Ser  
 365 370 375  
 Gly Asp Asn Tyr Arg Gly Gln Gly Ser Ser Trp Gly Ser Gly Gly  
 380 385 390  
 Gly Asp Ala Val Gly Gly Val Asn Thr Val Asn Ser Glu Thr Ser  
 395 400 405  
 Pro Gly Met Phe Asn Phe Asp Thr Phe Trp Lys Asn Phe Lys Ser  
 410 415 420  
 Lys Leu Gly Phe Ile Asn Trp Asp Ala Ile Asn Lys Asp Gln Arg  
 425 430 435  
 Ser Ser Arg Ile Pro  
 440

<210> 53  
 <211> 3580  
 <212> DNA  
 <213> Homo sapiens

<400> 53  
 gaccgggtccc tccgggtcctg gatgtgcgga ctctgctgca gcgagggctg 50  
 caggcccgcc gggcggtgct caccgtgccc tggctggtgg agtttctctc 100  
 ctttctgtgac catgttggtc ctttctgtga atattaccgg gacatcttca 150  
 ctctcctgct gcgcctgcac cggagcttgg tgttgtcgca ggagagttag 200  
 gggaagatgt gtttcctgaa caagctgctg ctacttctg tcttgggctg 250  
 gcttttccag attccacag tccctgagga cttgttcttt ctggaagagg 300  
 gtccctcata tgcctttgag gtggacacag tagccccaga gcatggcttg 350  
 gacaatgcgc ctgtggtgga ccagcagctg ctctacacct gctgccccta 400  
 catcggagag ctccggaaac tgctcgcttc gtgggtgtca ggcagtagtg 450  
 gacggagtgg gggcttcatg aggaaaatca cccccaccac taccaccagc 500  
 ctgggagccc agccttccca gaccagccag gggctgcagg cacagctcgc 550  
 ccaggccttt ttccacaacc agccgccctc cttgcgccgg accgtagagt 600  
 tcgtggcaga aagaattgga tcaaactgtg tcaaacatat caaggctaca 650  
 ctggtggcag atctggtgcg ccaggcagag tcaacttctcc aagagcagct 700  
 ggtgacacag ggagaggaag ggggagaccc agcccagctg ttggagatct 750  
 tgtgttccca gctgtgccct cacggggccc aggcattggc cctggggcgg 800

gagttctgtc aaaggaagag ccctggggct gtgcggggcg tgcttccaga 850  
 ggagaccccg gcagccgttc tgagcagtgc agagaacatt gctgtggggc 900  
 ttgcaacaga gaaagcctgt gcttggctgt cagccaacat cacagcactg 950  
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<211> 280

<212> PRT

<213> Homo sapiens

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His	Gly	Leu	Asp	Asn	Ala	Pro	Val	Val	Asp	Gln	Gln	Leu	Leu	Tyr
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Thr	Cys	Cys	Pro	Tyr	Ile	Gly	Glu	Leu	Arg	Lys	Leu	Leu	Ala	Ser
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Val	Thr	Gln	Gly	Glu	Glu	Gly	Gly	Asp	Pro	Ala	Gln	Leu	Leu	Glu
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Ile	Leu	Cys	Ser	Gln	Leu	Cys	Pro	His	Gly	Ala	Gln	Ala	Leu	Ala
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Leu	Gly	Arg	Glu	Phe	Cys	Gln	Arg	Lys	Ser	Pro	Gly	Ala	Val	Arg
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Leu	Ser	Ala	Asn	Ile	Thr	Ala	Leu	Ile	Arg	Arg	Glu	Val	Lys	Ala
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 <212> DNA  
 <213> Homo sapiens

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<210> 56

<211> 299

<212> PRT

<213> Homo sapiens

<400> 56

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				20					25					30

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Thr	Thr	Gly	Tyr	Ser	Ala	Asp	Val	Gly	Asn	Lys	Thr	Thr	Tyr	Arg		110	115	120
Val	Val	Ala	His	Ser	Ser	Val	Phe	Arg	Val	Leu	Arg	Arg	Pro	Gln		125	130	135
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Ile	Gln	Arg	Ala	Gly	Leu	Val	Phe	Pro	Asn	Met	Glu	Ala	Tyr	Ala		170	175	180
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Glu	Thr	Gly	Lys	Asp	Arg	Glu	Lys	Ser	His	Ser	Trp	Leu	Ser	Thr		200	205	210
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His	Val	Tyr	Gly	Met	Val	Pro	Pro	Asn	Tyr	Cys	Ser	Gln	Arg	Pro		230	235	240
Arg	Leu	Gln	Arg	Met	Pro	Tyr	His	Tyr	Tyr	Glu	Pro	Lys	Gly	Pro		245	250	255
Asp	Glu	Cys	Val	Thr	Tyr	Ile	Gln	Asn	Glu	His	Ser	Arg	Lys	Gly		260	265	270
Asn	His	His	Arg	Phe	Ile	Thr	Glu	Lys	Arg	Val	Phe	Ser	Ser	Trp		275	280	285
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<210> 57

<211> 4277

<212> DNA

<213> Homo sapiens

<400> 57

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<211> 1115

<212> PRT  
 <213> Homo sapiens

<400> 58

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Leu	Val	Ile	Thr	Ala	Leu	Asn	Asn	His	Thr	Val	Gly	Arg	Tyr	Gln	
				95					100					105	
Cys	Val	Ala	Arg	Met	Pro	Ala	Gly	Ala	Val	Ala	Ser	Val	Pro	Ala	
				110					115					120	
Thr	Val	Thr	Leu	Ala	Asn	Leu	Gln	Asp	Phe	Lys	Leu	Asp	Val	Gln	
				125					130					135	
His	Val	Ile	Glu	Val	Asp	Glu	Gly	Asn	Thr	Ala	Val	Ile	Ala	Cys	
				140					145					150	
His	Leu	Pro	Glu	Ser	His	Pro	Lys	Ala	Gln	Val	Arg	Tyr	Ser	Val	
				155					160					165	
Lys	Gln	Glu	Trp	Leu	Glu	Ala	Ser	Arg	Gly	Asn	Tyr	Leu	Ile	Met	
				170					175					180	
Pro	Ser	Gly	Asn	Leu	Gln	Ile	Val	Asn	Ala	Ser	Gln	Glu	Asp	Glu	
				185					190					195	
Gly	Met	Tyr	Lys	Cys	Ala	Ala	Tyr	Asn	Pro	Val	Thr	Gln	Glu	Val	
				200					205					210	
Lys	Thr	Ser	Gly	Ser	Ser	Asp	Arg	Leu	Arg	Val	Arg	Arg	Ser	Thr	
				215					220					225	
Ala	Glu	Ala	Ala	Arg	Ile	Ile	Tyr	Pro	Pro	Glu	Ala	Gln	Thr	Ile	
				230					235					240	
Ile	Val	Thr	Lys	Gly	Gln	Ser	Leu	Ile	Leu	Glu	Cys	Val	Ala	Ser	
				245					250					255	
Gly	Ile	Pro	Pro	Pro	Arg	Val	Thr	Trp	Ala	Lys	Asp	Gly	Ser	Ser	
				260					265					270	

Val Thr Gly Tyr	Asn Lys Thr Arg Phe	Leu Leu Ser Asn Leu	Leu
	275	280	285
Ile Asp Thr Thr	Ser Glu Glu Asp Ser	Gly Thr Tyr Arg Cys	Met
	290	295	300
Ala Asp Asn Gly	Val Gly Gln Pro Gly	Ala Ala Val Ile Leu	Tyr
	305	310	315
Asn Val Gln Val	Phe Glu Pro Pro Glu	Val Thr Met Glu Leu	Ser
	320	325	330
Gln Leu Val Ile	Pro Trp Gly Gln Ser	Ala Lys Leu Thr Cys	Glu
	335	340	345
Val Arg Gly Asn	Pro Pro Pro Ser Val	Leu Trp Leu Arg Asn	Ala
	350	355	360
Val Pro Leu Ile	Ser Ser Gln Arg Leu	Arg Leu Ser Arg Arg	Ala
	365	370	375
Leu Arg Val Leu	Ser Met Gly Pro Glu	Asp Glu Gly Val Tyr	Gln
	380	385	390
Cys Met Ala Glu	Asn Glu Val Gly Ser	Ala His Ala Val Val	Gln
	395	400	405
Leu Arg Thr Ser	Arg Pro Ser Ile Thr	Pro Arg Leu Trp Gln	Asp
	410	415	420
Ala Glu Leu Ala	Thr Gly Thr Pro Pro	Val Ser Pro Ser Lys	Leu
	425	430	435
Gly Asn Pro Glu	Gln Met Leu Arg Gly	Gln Pro Ala Leu Pro	Arg
	440	445	450
Pro Pro Thr Ser	Val Gly Pro Ala Ser	Pro Lys Cys Pro Gly	Glu
	455	460	465
Lys Gly Gln Gly	Ala Pro Ala Glu Ala	Pro Ile Ile Leu Ser	Ser
	470	475	480
Pro Arg Thr Ser	Lys Thr Asp Ser Tyr	Glu Leu Val Trp Arg	Pro
	485	490	495
Arg His Glu Gly	Ser Gly Arg Ala Pro	Ile Leu Tyr Tyr Val	Val
	500	505	510
Lys His Arg Lys	Gln Val Thr Asn Ser	Ser Asp Asp Trp Thr	Ile
	515	520	525
Ser Gly Ile Pro	Ala Asn Gln His Arg	Leu Thr Leu Thr Arg	Leu
	530	535	540
Asp Pro Gly Ser	Leu Tyr Glu Val Glu	Met Ala Ala Tyr Asn	Cys
	545	550	555
Ala Gly Glu Gly	Gln Thr Ala Met Val	Thr Phe Arg Thr Gly	Arg



	560		565		570
Arg Pro Lys Pro	Glu Ile Met Ala Ser	Lys Glu Gln Gln Ile	Gln		
	575	580	585		
Arg Asp Asp Pro	Gly Ala Ser Pro Gln	Ser Ser Ser Gln Pro	Asp		
	590	595	600		
His Gly Arg Leu	Ser Pro Pro Glu Ala	Pro Asp Arg Pro Thr	Ile		
	605	610	615		
Ser Thr Ala Ser	Glu Thr Ser Val Tyr	Val Thr Trp Ile Pro	Arg		
	620	625	630		
Gly Asn Gly Gly	Phe Pro Ile Gln Ser	Phe Arg Val Glu Tyr	Lys		
	635	640	645		
Lys Leu Lys Lys	Val Gly Asp Trp Ile	Leu Ala Thr Ser Ala	Ile		
	650	655	660		
Pro Pro Ser Arg	Leu Ser Val Glu Ile	Thr Gly Leu Glu Lys	Gly		
	665	670	675		
Thr Ser Tyr Lys	Phe Arg Val Arg Ala	Leu Asn Met Leu Gly	Glu		
	680	685	690		
Ser Glu Pro Ser	Ala Pro Ser Arg Pro	Tyr Val Val Ser Gly	Tyr		
	695	700	705		
Ser Gly Arg Val	Tyr Glu Arg Pro Val	Ala Gly Pro Tyr Ile	Thr		
	710	715	720		
Phe Thr Asp Ala	Val Asn Glu Thr Thr	Ile Met Leu Lys Trp	Met		
	725	730	735		
Tyr Ile Pro Ala	Ser Asn Asn Asn Thr	Pro Ile His Gly Phe	Tyr		
	740	745	750		
Ile Tyr Tyr Arg	Pro Thr Asp Ser Asp	Asn Asp Ser Asp Tyr	Lys		
	755	760	765		
Lys Asp Met Val	Glu Gly Asp Lys Tyr	Trp His Ser Ile Ser	His		
	770	775	780		
Leu Gln Pro Glu	Thr Ser Tyr Asp Ile	Lys Met Gln Cys Phe	Asn		
	785	790	795		
Glu Gly Gly Glu	Ser Glu Phe Ser Asn	Val Met Ile Cys Glu	Thr		
	800	805	810		
Lys Ala Arg Lys	Ser Ser Gly Gln Pro	Gly Arg Leu Pro Pro	Pro		
	815	820	825		
Thr Leu Ala Pro	Pro Gln Pro Pro Leu	Pro Glu Thr Ile Glu	Arg		
	830	835	840		
Pro Val Gly Thr	Gly Ala Met Val Ala	Arg Ser Ser Asp Leu	Pro		
	845	850	855		

Tyr Leu Ile Val Gly Val Val Leu Gly Ser Ile Val Leu Ile Ile  
 860 865 870  
 Val Thr Phe Ile Pro Phe Cys Leu Trp Arg Ala Trp Ser Lys Gln  
 875 880 885  
 Lys His Thr Thr Asp Leu Gly Phe Pro Arg Ser Ala Leu Pro Pro  
 890 895 900  
 Ser Cys Pro Tyr Thr Met Val Pro Leu Gly Gly Leu Pro Gly His  
 905 910 915  
 Gln Ala Ser Gly Gln Pro Tyr Leu Ser Gly Ile Ser Gly Arg Ala  
 920 925 930  
 Cys Ala Asn Gly Ile His Met Asn Arg Gly Cys Pro Ser Ala Ala  
 935 940 945  
 Val Gly Tyr Pro Gly Met Lys Pro Gln Gln His Cys Pro Gly Glu  
 950 955 960  
 Leu Gln Gln Gln Ser Asp Thr Ser Ser Leu Leu Arg Gln Thr His  
 965 970 975  
 Leu Gly Asn Gly Tyr Asp Pro Gln Ser His Gln Ile Thr Arg Gly  
 980 985 990  
 Pro Lys Ser Ser Pro Asp Glu Gly Ser Phe Leu Tyr Thr Leu Pro  
 995 1000 1005  
 Asp Asp Ser Thr His Gln Leu Leu Gln Pro His His Asp Cys Cys  
 1010 1015 1020  
 Gln Arg Gln Glu Gln Pro Ala Ala Val Gly Gln Ser Gly Val Arg  
 1025 1030 1035  
 Arg Ala Pro Asp Ser Pro Val Leu Glu Ala Val Trp Asp Pro Pro  
 1040 1045 1050  
 Phe His Ser Gly Pro Pro Cys Cys Leu Gly Leu Val Pro Val Glu  
 1055 1060 1065  
 Glu Val Asp Ser Pro Asp Ser Cys Gln Val Ser Gly Gly Asp Trp  
 1070 1075 1080  
 Cys Pro Gln His Pro Val Gly Ala Tyr Val Gly Gln Glu Pro Gly  
 1085 1090 1095  
 Met Gln Leu Ser Pro Gly Pro Leu Val Arg Val Ser Phe Glu Thr  
 1100 1105 1110  
 Pro Pro Leu Thr Ile  
 1115

<210> 59  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 59  
 gggaaacaca gcagtcattg cctgc 25

<210> 60  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 60  
 gcacacgtag cctgtcgtg gagg 24

<210> 61  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 61  
 caccacaaag cccaggtccg gtacagcgtc aaacaagagt gg 42

<210> 62  
 <211> 1661  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 678  
 <223> unknown base

<400> 62  
 cgggaggctg ggtcgtcatg atccggaccc cattgtcggc ctctgcccatt 50  
 cgcctgctcc tcccaggctc ccgcgccga cccccgcgca acatgcagcc 100  
 caaggccgc gagggttccc gcgcgctcag ccggcggtat ctgcggcgtc 150  
 tgctgctcct gctactgctg ctgctgctgc ggcagcccggt aaccgcgcg 200  
 gagaccacgc cgggcgcccc cagagccctc tccacgctgg gctccccag 250  
 cctcttcacc acgcgggtg tcccagcgc cctcactacc ccaggcctca 300  
 ctacgccagg ccccccaaa accctggacc ttcgggggtc gcgcaggcc 350

ctgatgcgga gtttccact cgtggacggc cacaatgacc tgccccaggt 400  
cctgagacag cgttacaaga atgtgcttca ggatgttaac ctgcgaaatt 450  
tcagccatgg tcagaccagc ctggacaggc ttagagacgg cctcgtgggt 500  
gccagttct ggtcagcctc cgtctcatgc cagtcccagg accagactgc 550  
cgtgcgcctc gccctggagc agattgacct cattcaccgc atgtgtgcct 600  
cctactctga actogagctt gtgacctcag ctgaaggctt gaacagctct 650  
caaaagctgg cctgcctcat tggcgtgnag ggtggtcact cactggacag 700  
cagcctctct gtgtgcgca gtttctatgt gctgggggtg cgctacctga 750  
cacttacctt cacctgcagt acaccatggg cagagagttc caccaagttc 800  
agacaccaca tgtacaccaa cgtcagcggg ttgacaagct ttggtgagaa 850  
agtagtagag gagttgaacc gcttgggcat gatgatagat ttgtcctatg 900  
catcggacac cttgataaga agggctctgg aagtgtctca ggctcctgtg 950  
atcttctccc actcagctgc cagagctgtg tgtgacaatt tgttgaatgt 1000  
tcccgatgat atcctgcagc ttctgaagaa cgggtggcatc gtgatgggtg 1050  
cactgtccat ggggggtgctg cagtgaacc tgcttgctaa cgtgtccact 1100  
gtggcagatc actttgacca catcagggca gtcattggat ctgagttcat 1150  
cgggattggg ggaaattatg acgggactgg ccggttccct caggggctgg 1200  
aggatgtgtc cacataccca gtctgatag aggagttgct gagtcgtasc 1250  
tggagcgagg aagagcttca aggtgtcctt cgtggaaacc tgctgcgggt 1300  
cttcagacaa gtggaaaagg tgagagagga gagcagggcg cagagccccg 1350  
tggaggctga gtttccatat gggcaactga gcacatctg ccactccac 1400  
ctcgtgcctc agaatggaca ccaggctact catctggagg tgaccaagca 1450  
gccaaccaat cgggtcccct ggaggctcctc aaatgcctcc ccatacctg 1500  
ttccaggcct tgtggctgct gccaccatcc caaccttcac ccagtggctc 1550  
tgctgacaca gtcgggtcccc gcagaggcca ctgtggcaaa gcctcacaaa 1600  
gccccctctc ctagtgcatt cacaagcata tgctgagaat aaacatgtta 1650  
cacatggaaa a 1661

<210> 63  
<211> 487  
<212> PRT  
<213> Homo sapiens

<220>  
 <221> unsure  
 <222> 196, 386  
 <223> unknown amino acid

<400> 63

Met	Gln	Pro	Thr	Gly	Arg	Glu	Gly	Ser	Arg	Ala	Leu	Ser	Arg	Arg	
1				5					10					15	
Tyr	Leu	Arg	Arg	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Leu	Arg	
				20					25					30	
Gln	Pro	Val	Thr	Arg	Ala	Glu	Thr	Thr	Pro	Gly	Ala	Pro	Arg	Ala	
				35					40					45	
Leu	Ser	Thr	Leu	Gly	Ser	Pro	Ser	Leu	Phe	Thr	Thr	Pro	Gly	Val	
				50					55					60	
Pro	Ser	Ala	Leu	Thr	Thr	Pro	Gly	Leu	Thr	Thr	Pro	Gly	Thr	Pro	
				65					70					75	
Lys	Thr	Leu	Asp	Leu	Arg	Gly	Arg	Ala	Gln	Ala	Leu	Met	Arg	Ser	
				80					85					90	
Phe	Pro	Leu	Val	Asp	Gly	His	Asn	Asp	Leu	Pro	Gln	Val	Leu	Arg	
				95					100					105	
Gln	Arg	Tyr	Lys	Asn	Val	Leu	Gln	Asp	Val	Asn	Leu	Arg	Asn	Phe	
				110					115					120	
Ser	His	Gly	Gln	Thr	Ser	Leu	Asp	Arg	Leu	Arg	Asp	Gly	Leu	Val	
				125					130					135	
Gly	Ala	Gln	Phe	Trp	Ser	Ala	Ser	Val	Ser	Cys	Gln	Ser	Gln	Asp	
				140					145					150	
Gln	Thr	Ala	Val	Arg	Leu	Ala	Leu	Glu	Gln	Ile	Asp	Leu	Ile	His	
				155					160					165	
Arg	Met	Cys	Ala	Ser	Tyr	Ser	Glu	Leu	Glu	Leu	Val	Thr	Ser	Ala	
				170					175					180	
Glu	Gly	Leu	Asn	Ser	Ser	Gln	Lys	Leu	Ala	Cys	Leu	Ile	Gly	Val	
				185					190					195	
Xaa	Gly	Gly	His	Ser	Leu	Asp	Ser	Ser	Leu	Ser	Val	Leu	Arg	Ser	
				200					205					210	
Phe	Tyr	Val	Leu	Gly	Val	Arg	Tyr	Leu	Thr	Leu	Thr	Phe	Thr	Cys	
				215					220					225	
Ser	Thr	Pro	Trp	Ala	Glu	Ser	Ser	Thr	Lys	Phe	Arg	His	His	Met	
				230					235					240	
Tyr	Thr	Asn	Val	Ser	Gly	Leu	Thr	Ser	Phe	Gly	Glu	Lys	Val	Val	
				245					250					255	
Glu	Glu	Leu	Asn	Arg	Leu	Gly	Met	Met	Ile	Asp	Leu	Ser	Tyr	Ala	

	260	265	270
Ser Asp Thr Leu	Ile Arg Arg Val Leu	Glu Val Ser Gln Ala	Pro
	275	280	285
Val Ile Phe Ser	His Ser Ala Ala Arg	Ala Val Cys Asp Asn	Leu
	290	295	300
Leu Asn Val Pro	Asp Asp Ile Leu Gln	Leu Leu Lys Asn Gly	Gly
	305	310	315
Ile Val Met Val	Thr Leu Ser Met Gly	Val Leu Gln Cys Asn	Leu
	320	325	330
Leu Ala Asn Val	Ser Thr Val Ala Asp	His Phe Asp His Ile	Arg
	335	340	345
Ala Val Ile Gly	Ser Glu Phe Ile Gly	Ile Gly Gly Asn Tyr	Asp
	350	355	360
Gly Thr Gly Arg	Phe Pro Gln Gly Leu	Glu Asp Val Ser Thr	Tyr
	365	370	375
Pro Val Leu Ile	Glu Glu Leu Leu Ser	Arg Xaa Trp Ser Glu	Glu
	380	385	390
Glu Leu Gln Gly	Val Leu Arg Gly Asn	Leu Leu Arg Val Phe	Arg
	395	400	405
Gln Val Glu Lys	Val Arg Glu Glu Ser	Arg Ala Gln Ser Pro	Val
	410	415	420
Glu Ala Glu Phe	Pro Tyr Gly Gln Leu	Ser Thr Ser Cys His	Ser
	425	430	435
His Leu Val Pro	Gln Asn Gly His Gln	Ala Thr His Leu Glu	Val
	440	445	450
Thr Lys Gln Pro	Thr Asn Arg Val Pro	Trp Arg Ser Ser Asn	Ala
	455	460	465
Ser Pro Tyr Leu	Val Pro Gly Leu Val	Ala Ala Ala Thr Ile	Pro
	470	475	480
Thr Phe Thr Gln	Trp Leu Cys		
	485		

<210> 64

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 64

ccttcacctg cagtacacca tgggc 25

<210> 65

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 65

gtcacacaca gctctggcag ctgag 25

<210> 66

<211> 47

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-47

<223> Synthetic construct.

<400> 66

ccaagtctag acaccacatg tacaccaacg tcagcggatt gacaagc 47

<210> 67

<211> 1564

<212> DNA

<213> Homo sapiens

<400> 67

tgctaggctc tgtcccacaa tgcacccgag agcaggagct gaaagcctct 50

aacaccacaca gatccctcta tgactgcaat gtgaggtgtc cggctttgct 100

ggcccagcaa gcctgataag catgaagctc ttatctttgg tggctgtggt 150

cgggtgtttg ctggtgcccc cagctgaagc caacaagagt tctgaagata 200

tccggtgcaa atgcatctgt ccaccttata gaaacatcag tgggcacatt 250

tacaaccaga atgtatccca gaaggactgc aactgcctgc acgtggtgga 300

gcccattgcca gtgcctggcc atgacgtgga ggcctactgc ctgctgtgcg 350

agtgcaggta cgaggagcgc agcaccacca ccatcaaggt catcattgtc 400

atctacctgt ccgtggtggg tgccctggtg ctctacatgg ccttcctgat 450

gctggtggac cctctgatcc gaaagccgga tgcatacact gagcaactgc 500

acaatgagga ggagaatgag gatgctcgct ctatggcagc agctgctgca 550

tccctcgggg gaccccgagc aaacacagtc ctggagcgtg tggaaggtgc 600

ccagcagcgg tggaagctgc aggtgcagga gcagcgggaag acagtcttcg 650  
atcggcacaa gatgctcagc tagatgggct ggtgtggttg ggtcaaggcc 700  
ccaacaccat ggctgccagc ttccaggctg gacaaagcag ggggctactt 750  
ctcccttccc tcggttccag tcttcccttt aaaagcctgt ggcatttttc 800  
ctccttctcc ctaactttag aaatgttgta cttggctatt ttgattaggg 850  
aagaggggatg tggctctctga tctctgttgt cttcttgggt ctttgggggt 900  
gaagggaggg ggaaggcagg ccagaaggga atggagacat tcgaggcggc 950  
ctcaggagtg gatgcgatct gtctctcctg gctccactct tgccgccttc 1000  
cagctctgag tcttgggaat gttgttacct ttggaagata aagctgggtc 1050  
ttcaggaact cagtgtctgg gaggaagca tggcccagca ttcagcatgt 1100  
gttcctttct gcagtgggtc ttatcaccac ctccctcca gccccggcgc 1150  
ctcagcccca gcccagctc cagccctgag gacagctctg atgggagagc 1200  
tgggccccct gagcccactg ggtcttcagg gtgcaactgga agctgggtgt 1250  
cgctgtcccc tgtgcacttc tcgcaactgg gcattggagt cccatgcata 1300  
ctctgctgcc ggtcccctca cctgcaactg aggggtcttg gcagtccttc 1350  
ctctccccag tgtccacagt cactgagcca gacggtcggt tggaacatga 1400  
gactcgaggc tgagcgtgga tctgaacacc acagcccctg tacttgggtt 1450  
gcctcttgct cctgaacttc gttgtaccag tgcattggaga gaaaattttg 1500  
tcctcttgct ttagagttgt gtgtaaatac aggaagccat cattaaattg 1550  
ttttatttct ctca 1564

<210> 68  
<211> 183  
<212> PRT  
<213> Homo sapiens

<400> 68  
Met Lys Leu Leu Ser Leu Val Ala Val Val Gly Cys Leu Leu Val  
1 5 10 15  
Pro Pro Ala Glu Ala Asn Lys Ser Ser Glu Asp Ile Arg Cys Lys  
20 25 30  
Cys Ile Cys Pro Pro Tyr Arg Asn Ile Ser Gly His Ile Tyr Asn  
35 40 45  
Gln Asn Val Ser Gln Lys Asp Cys Asn Cys Leu His Val Val Glu  
50 55 60



Pro	Met	Pro	Val	Pro	Gly	His	Asp	Val	Glu	Ala	Tyr	Cys	Leu	Leu
				65					70					75
Cys	Glu	Cys	Arg	Tyr	Glu	Glu	Arg	Ser	Thr	Thr	Thr	Ile	Lys	Val
				80					85					90
Ile	Ile	Val	Ile	Tyr	Leu	Ser	Val	Val	Gly	Ala	Leu	Leu	Leu	Tyr
				95					100					105
Met	Ala	Phe	Leu	Met	Leu	Val	Asp	Pro	Leu	Ile	Arg	Lys	Pro	Asp
				110					115					120
Ala	Tyr	Thr	Glu	Gln	Leu	His	Asn	Glu	Glu	Glu	Asn	Glu	Asp	Ala
				125					130					135
Arg	Ser	Met	Ala	Ala	Ala	Ala	Ala	Ser	Leu	Gly	Gly	Pro	Arg	Ala
				140					145					150
Asn	Thr	Val	Leu	Glu	Arg	Val	Glu	Gly	Ala	Gln	Gln	Arg	Trp	Lys
				155					160					165
Leu	Gln	Val	Gln	Glu	Gln	Arg	Lys	Thr	Val	Phe	Asp	Arg	His	Lys
				170					175					180

Met Leu Ser

<210> 69  
 <211> 3170  
 <212> DNA  
 <213> Homo sapiens

<400> 69  
 agcgggtctc gcttgggttc cgctaatttc tgtcctgagg cgtgagactg 50  
 agttcatagg gtcctgggtc cccgaaccag gaagggttga gggaacacaa 100  
 tctgcaagcc cccgcgaccc aagtgagggg ccccggtgtg gggctctccc 150  
 tccctttgca ttcccacccc tccgggcttt gcgctcttct ggggaccccc 200  
 tcgccgggag atggccgcgt tgatgcggag caaggattcg tctgctgcc 250  
 tgctcctact ggccgcggtg ctgatggtgg agagctcaca gatcggcagt 300  
 tcgcgggcca aactcaactc catcaagtcc tctctgggcg gggagacgcc 350  
 tggtcaggcc gccaatcgat ctgcgggcat gtaccaagga ctggcattcg 400  
 gcggcagtaa gaagggcaaa aacctggggc aggcctaccc ttgtagcagt 450  
 gataaggagt gtgaagttgg gaggtattgc cacagtcccc accaaggatc 500  
 atcggcctgc atggtgtgtc ggagaaaaaa gaagcgtgc caccgagatg 550  
 gcatgtgctg cccagtagcc cgctgcaata atggcatctg tatccagtt 600  
 actgaaagca tcttaacccc tcacatccc gctctggatg gtactcggca 650

cagagatcga aaccacggtc attactcaaa ccatgacttg ggatggcaga 700  
atctaggaag accacacact aagatgtcac atataaaagg gcatgaagga 750  
gacccctgcc tacgatcatc agactgcatt gaagggtttt gctgtgctcg 800  
tcatttctgg accaaaaatct gcaaaccagt gctccatcag ggggaagtct 850  
gtaccaaaaca acgcaagaag ggttctcatg ggctggaaat tttccagcgt 900  
tgcgactgtg cgaagggcct gtcttgcaaa gtatggaaag atgccaccta 950  
ctcctccaaa gccagactcc atgtgtgtca gaaaatttga tcaccattga 1000  
ggaacatcat caattgcaga ctgtgaagtt gtgtatttaa tgcattatag 1050  
catggtggaa aataaggttc agatgcagaa gaatggctaa aataagaaac 1100  
gtgataagaa tatagatgat cacaaaaagg gagaaagaaa acatgaactg 1150  
aatagattag aatgggtgac aaatgcagtg cagccagtgt ttccattatg 1200  
caacttgtct atgtaaataa tgtacacatt tgtggaaaat gctattatta 1250  
agagaacaag cacacagtgg aaattactga tgagtagcat gtgactttcc 1300  
aagagtttag gttgtgctgg aggagagggtt tccttcagat tgctgattgc 1350  
ttatacaaat aacctacatg ccagatttct attcaacgtt agagtttaac 1400  
aaaatactcc tagaataact tgttatacaa taggttctaa aaataaaatt 1450  
gctaaacaag aaatgaaaac atggagcatt gttaatttac aacagaaaat 1500  
taccttttga tttgtaacac tacttctgct gttcaatcaa gagtcttggt 1550  
agataagaaa aaaatcagtc aatatttcca aataattgca aaataatggc 1600  
cagttgttta ggaaggcctt taggaagaca aataaataac aaacaaacag 1650  
ccacaaatac ttttttttca aaatttttagt tttacctgta attaataaga 1700  
actgatacaa gacaaaaaca gttccttcag attctacgga atgacagtat 1750  
atctctcttt atcctatgtg attcctgctc tgaatgcatt atattttcca 1800  
aactataccc ataaattgtg actagtaaaa tacttacaca gagcagaatt 1850  
ttcacagatg gcaaaaaaat ttaaagatgt ccaatatatg tgggaaaaga 1900  
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agattgagtt tgagcctgta tatctattaa aaatttcaac ttcccacata 2750  
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<210> 70

<211> 259

<212> PRT

<213> Homo sapiens

<400> 70

Met	Ala	Ala	Leu	Met	Arg	Ser	Lys	Asp	Ser	Ser	Cys	Cys	Leu	Leu
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Leu	Leu	Ala	Ala	Val	Leu	Met	Val	Glu	Ser	Ser	Gln	Ile	Gly	Ser
				20					25					30

Ser	Arg	Ala	Lys	Leu	Asn	Ser	Ile	Lys	Ser	Ser	Leu	Gly	Gly	Glu
				35					40					45

Thr	Pro	Gly	Gln	Ala	Ala	Asn	Arg	Ser	Ala	Gly	Met	Tyr	Gln	Gly	
				50					55					60	
Leu	Ala	Phe	Gly	Gly	Ser	Lys	Lys	Gly	Lys	Asn	Leu	Gly	Gln	Ala	
				65					70					75	
Tyr	Pro	Cys	Ser	Ser	Asp	Lys	Glu	Cys	Glu	Val	Gly	Arg	Tyr	Cys	
				80					85					90	
His	Ser	Pro	His	Gln	Gly	Ser	Ser	Ala	Cys	Met	Val	Cys	Arg	Arg	
				95					100					105	
Lys	Lys	Lys	Arg	Cys	His	Arg	Asp	Gly	Met	Cys	Cys	Pro	Ser	Thr	
				110					115					120	
Arg	Cys	Asn	Asn	Gly	Ile	Cys	Ile	Pro	Val	Thr	Glu	Ser	Ile	Leu	
				125					130					135	
Thr	Pro	His	Ile	Pro	Ala	Leu	Asp	Gly	Thr	Arg	His	Arg	Asp	Arg	
				140					145					150	
Asn	His	Gly	His	Tyr	Ser	Asn	His	Asp	Leu	Gly	Trp	Gln	Asn	Leu	
				155					160					165	
Gly	Arg	Pro	His	Thr	Lys	Met	Ser	His	Ile	Lys	Gly	His	Glu	Gly	
				170					175					180	
Asp	Pro	Cys	Leu	Arg	Ser	Ser	Asp	Cys	Ile	Glu	Gly	Phe	Cys	Cys	
				185					190					195	
Ala	Arg	His	Phe	Trp	Thr	Lys	Ile	Cys	Lys	Pro	Val	Leu	His	Gln	
				200					205					210	
Gly	Glu	Val	Cys	Thr	Lys	Gln	Arg	Lys	Lys	Gly	Ser	His	Gly	Leu	
				215					220					225	
Glu	Ile	Phe	Gln	Arg	Cys	Asp	Cys	Ala	Lys	Gly	Leu	Ser	Cys	Lys	
				230					235					240	
Val	Trp	Lys	Asp	Ala	Thr	Tyr	Ser	Ser	Lys	Ala	Arg	Leu	His	Val	
				245					250					255	

Cys Gln Lys Ile

<210> 71  
 <211> 1809  
 <212> DNA  
 <213> Homo sapiens

<400> 71  
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 acatcacgtt tttaaaaatt gatttcttca aattcatggc aaatatttcc 150  
 cttcccttta acttcttatg tcagaatgag gaaggatagc tgcatttatt 200

tagtcagttt tcattgcata gtaatatatt catgtagtat tttctaagtt 250  
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 gtacacagca gaatagtaca agtcacccta caactactac ttcttgggac 550  
 ctcaagcccc caacatoccc gtccctcagtc ctccagtcac ttgacttcaa 600  
 atctcaacct gagccatccc cagttcttag ccagttgagc cagcgacaac 650  
 agcaccagag ccaggcagtc actgttcctc ctccctggtt ggagtccttt 700  
 ccttcccagg caaaacttcg agaatcaaca cctggagaca gtccctccac 750  
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 aatcagattc ccatcagctt gtattcgaag tctttaagtg agcctttgaa 1050  
 tacatcttta tcaatgacca gtgcagtaca gaactccaca tatacaactt 1100  
 ccgtcattac ctccctcagc ctgacaagct catcactgaa ttctgctagt 1150  
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 cccataccaa agccctgtga gttcatcaga gtcagctcca ggaaccatca 1250  
 tgaatggaca tgggtgggtg cgaagtcagc agacactaga cagtaagtat 1300  
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 aaaaagcagc ccttttgcct ttttgttttt ggaccagggtg ttggctgtgg 1450  
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 ctttgggggg ccaaggcagg cagattgccc aagctcagga gtttgagacc 1650

accctgggca acatggtgaa actctgtctc tactaaaata cgaaaaacta 1700  
gccgggtgtg gtggcggcgc gtgcctgtaa tcccagctac ttgggaggct 1750  
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ctgaaaaga 1809

<210> 72  
<211> 363  
<212> PRT  
<213> Homo sapiens

<400> 72  
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Cys Ser Phe Ile Pro Leu Leu Lys Ser Ser Val Leu Gly Ser Gly  
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Phe Gly Glu Leu Ala Pro Pro Lys Met Ala Asn Ile Thr Ser Ser  
35 40 45  
Gln Ile Leu Asp Gln Leu Lys Ala Pro Ser Leu Gly Gln Phe Thr  
50 55 60  
Thr Thr Pro Ser Thr Gln Gln Asn Ser Thr Ser His Pro Thr Thr  
65 70 75  
Thr Thr Ser Trp Asp Leu Lys Pro Pro Thr Ser Gln Ser Ser Val  
80 85 90  
Leu Ser His Leu Asp Phe Lys Ser Gln Pro Glu Pro Ser Pro Val  
95 100 105  
Leu Ser Gln Leu Ser Gln Arg Gln Gln His Gln Ser Gln Ala Val  
110 115 120  
Thr Val Pro Pro Pro Gly Leu Glu Ser Phe Pro Ser Gln Ala Lys  
125 130 135  
Leu Arg Glu Ser Thr Pro Gly Asp Ser Pro Ser Thr Val Asn Lys  
140 145 150  
Leu Leu Gln Leu Pro Ser Thr Thr Ile Glu Asn Ile Ser Val Ser  
155 160 165  
Val His Gln Pro Gln Pro Lys His Ile Lys Leu Ala Lys Arg Arg  
170 175 180  
Ile Pro Pro Ala Ser Lys Ile Pro Ala Ser Ala Val Glu Met Pro  
185 190 195  
Gly Ser Ala Asp Val Thr Gly Leu Asn Val Gln Phe Gly Ala Leu  
200 205 210  
Glu Phe Gly Ser Glu Pro Ser Leu Ser Glu Phe Gly Ser Ala Pro  
215 220 225

Ser Ser Glu Asn	Ser Asn Gln Ile Pro	Ile Ser Leu Tyr Ser	Lys
230	235	240	
Ser Leu Ser Glu	Pro Leu Asn Thr Ser	Leu Ser Met Thr Ser	Ala
245	250	255	
Val Gln Asn Ser	Thr Tyr Thr Thr Ser	Val Ile Thr Ser Cys	Ser
260	265	270	
Leu Thr Ser Ser	Ser Leu Asn Ser Ala	Ser Pro Val Ala Met	Ser
275	280	285	
Ser Ser Tyr Asp	Gln Ser Ser Val His	Asn Arg Ile Pro Tyr	Gln
290	295	300	
Ser Pro Val Ser	Ser Ser Glu Ser Ala	Pro Gly Thr Ile Met	Asn
305	310	315	
Gly His Gly Gly	Gly Arg Ser Gln Gln	Thr Leu Asp Ser Lys	Tyr
320	325	330	
Ser Ser Lys Leu	Leu Leu Ser Trp Leu	Val Pro Thr Lys Gln	Arg
335	340	345	
Lys Arg Ile Ala	His Val Met Trp Lys	Thr Pro Val Gly Gln	Trp
350	355	360	

Leu Ile Arg

<210> 73  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 73  
 aattcatggc aaatatttcc cttccc 26

<210> 74  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 74  
 tggtaaaactg gcccaaactc gg 22

<210> 75  
 <211> 50

<212> DNA  
<213> Artificial

<220>  
<221> Artificial sequence  
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<223> Synthetic construct

<400> 75  
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<210> 76  
<211> 1989  
<212> DNA  
<213> Homo sapiens

<400> 76  
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tgcaactcagc ggtggaggag acggacgcgg ggctgtacac ctgcaacctg 150  
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gctagattac aaaaacaaca tcctgaagga gagggcgag ctggcccaca 1000  
gccccctgcc tgccaagtac atcgacctag acaaagggtt ccggaaggag 1050











Tyr	Leu	Ala	Val	Ala	Ser	Thr	Val	Pro	Ser	Met	Leu	Cys	Leu	Val	110	115	120
Ala	Asn	Phe	Leu	Leu	Val	Asn	Arg	Val	Ala	Val	His	Ile	Arg	Val	125	130	135
Leu	Ala	Ser	Leu	Thr	Val	Ile	Leu	Ala	Ile	Phe	Met	Val	Ile	Thr	140	145	150
Ala	Leu	Val	Lys	Val	Asp	Thr	Ser	Ser	Trp	Thr	Arg	Gly	Phe	Phe	155	160	165
Ala	Val	Thr	Ile	Val	Cys	Met	Val	Ile	Leu	Ser	Gly	Ala	Ser	Thr	170	175	180
Val	Phe	Ser	Ser	Ser	Ile	Tyr	Gly	Met	Thr	Gly	Ser	Phe	Pro	Met	185	190	195
Arg	Asn	Ser	Gln	Ala	Leu	Ile	Ser	Gly	Gly	Ala	Met	Gly	Gly	Thr	200	205	210
Val	Ser	Ala	Val	Ala	Ser	Leu	Val	Asp	Leu	Ala	Ala	Ser	Ser	Asp	215	220	225
Val	Arg	Asn	Ser	Ala	Leu	Ala	Phe	Phe	Leu	Thr	Ala	Thr	Ile	Phe	230	235	240
Leu	Val	Leu	Cys	Met	Gly	Leu	Tyr	Leu	Leu	Leu	Ser	Arg	Leu	Glu	245	250	255
Tyr	Ala	Arg	Tyr	Tyr	Met	Arg	Pro	Val	Leu	Ala	Ala	His	Val	Phe	260	265	270
Ser	Gly	Glu	Glu	Glu	Leu	Pro	Gln	Asp	Ser	Leu	Ser	Ala	Pro	Ser	275	280	285
Val	Ala	Ser	Arg	Phe	Ile	Asp	Ser	His	Thr	Pro	Pro	Leu	Arg	Pro	290	295	300
Ile	Leu	Lys	Lys	Thr	Ala	Ser	Leu	Gly	Phe	Cys	Val	Thr	Tyr	Val	305	310	315
Phe	Phe	Ile	Thr	Ser	Leu	Ile	Tyr	Pro	Ala	Val	Cys	Thr	Asn	Ile	320	325	330
Glu	Ser	Leu	Asn	Lys	Gly	Ser	Gly	Ser	Leu	Trp	Thr	Thr	Lys	Phe	335	340	345
Phe	Ile	Pro	Leu	Thr	Thr	Phe	Leu	Leu	Tyr	Asn	Phe	Ala	Asp	Leu	350	355	360
Cys	Gly	Arg	Gln	Leu	Thr	Ala	Trp	Ile	Gln	Val	Pro	Gly	Pro	Asn	365	370	375
Ser	Lys	Ala	Leu	Pro	Gly	Phe	Val	Leu	Leu	Arg	Thr	Cys	Leu	Ile	380	385	390
Pro	Leu	Phe	Val	Leu	Cys	Asn	Tyr	Gln	Pro	Arg	Val	His	Leu	Lys			

395	400	405
Thr Val Val Phe Gln Ser Asp Val Tyr	Pro Ala Leu Leu Ser Ser	
410	415	420
Leu Leu Gly Leu Ser Asn Gly Tyr Leu	Ser Thr Leu Ala Leu Leu	
425	430	435
Tyr Gly Pro Lys Ile Val Pro Arg Glu	Leu Ala Glu Ala Thr Gly	
440	445	450
Val Val Met Ser Phe Tyr Val Cys Leu	Gly Leu Thr Leu Gly Ser	
455	460	465
Ala Cys Ser Thr Leu Leu Val His Leu	Ile	
470	475	

<210> 80  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 80  
 ttttgcggtc accattgtct gc 22

<210> 81  
 <211> 23  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> Artificial sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 81  
 cgtaggtgac acagaagccc agg 23

<210> 82  
 <211> 49  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial sequence  
 <222> 1-49  
 <223> Synthetic construct.

<400> 82  
 tacggcatga ccggctcctt tcctatgagg aactcccagg cactgatat 49

<210> 83  
 <211> 1844

<212> DNA  
<213> Homo sapiens

<400> 83

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 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaa 1844

<210> 84  
 <211> 567  
 <212> PRT  
 <213> Homo sapiens

<400> 84  
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 Asp Pro Phe Glu Lys Cys Met Gln Asp Pro Asp Tyr Glu Gln Leu  
 35 40 45  
 Leu Lys Val Val Thr Trp Gly Leu Asn Arg Thr Leu Lys Pro Gln  
 50 55 60  
 Arg Val Ile Val Val Gly Ala Gly Val Ala Gly Leu Val Ala Ala  
 65 70 75  
 Lys Val Leu Ser Asp Ala Gly His Lys Val Thr Ile Leu Glu Ala  
 80 85 90  
 Asp Asn Arg Ile Gly Gly Arg Ile Phe Thr Tyr Arg Asp Gln Asn  
 95 100 105  
 Thr Gly Trp Ile Gly Glu Leu Gly Ala Met Arg Met Pro Ser Ser  
 110 115 120  
 His Arg Ile Leu His Lys Leu Cys Gln Gly Leu Gly Leu Asn Leu  
 125 130 135  
 Thr Lys Phe Thr Gln Tyr Asp Lys Asn Thr Trp Thr Glu Val His  
 140 145 150  
 Glu Val Lys Leu Arg Asn Tyr Val Val Glu Lys Val Pro Glu Lys  
 155 160 165



Leu Gly Tyr Ala	Leu Arg Pro Gln Glu Lys Gly His Ser Pro Glu	170	175	180
Asp Ile Tyr Gln	Met Ala Leu Asn Gln Ala Leu Lys Asp Leu Lys	185	190	195
Ala Leu Gly Cys	Arg Lys Ala Met Lys Lys Phe Glu Arg His Thr	200	205	210
Leu Leu Glu Tyr	Leu Leu Gly Glu Gly Asn Leu Ser Arg Pro Ala	215	220	225
Val Gln Leu Leu	Gly Asp Val Met Ser Glu Asp Gly Phe Phe Tyr	230	235	240
Leu Ser Phe Ala	Glu Ala Leu Arg Ala His Ser Cys Leu Ser Asp	245	250	255
Arg Leu Gln Tyr	Ser Arg Ile Val Gly Gly Trp Asp Leu Leu Pro	260	265	270
Arg Ala Leu Leu	Ser Ser Leu Ser Gly Leu Val Leu Leu Asn Ala	275	280	285
Pro Val Val Ala	Met Thr Gln Gly Pro His Asp Val His Val Gln	290	295	300
Ile Glu Thr Ser	Pro Pro Ala Arg Asn Leu Lys Val Leu Lys Ala	305	310	315
Asp Val Val Leu	Leu Thr Ala Ser Gly Pro Ala Val Lys Arg Ile	320	325	330
Thr Phe Ser Pro	Pro Leu Pro Arg His Met Gln Glu Ala Leu Arg	335	340	345
Arg Leu His Tyr	Val Pro Ala Thr Lys Val Phe Leu Ser Phe Arg	350	355	360
Arg Pro Phe Trp	Arg Glu Glu His Ile Glu Gly Gly His Ser Asn	365	370	375
Thr Asp Arg Pro	Ser Arg Met Ile Phe Tyr Pro Pro Pro Arg Glu	380	385	390
Gly Ala Leu Leu	Leu Ala Ser Tyr Thr Trp Ser Asp Ala Ala Ala	395	400	405
Ala Phe Ala Gly	Leu Ser Arg Glu Glu Ala Leu Arg Leu Ala Leu	410	415	420
Asp Asp Val Ala	Ala Leu His Gly Pro Val Val Arg Gln Leu Trp	425	430	435
Asp Gly Thr Gly	Val Val Lys Arg Trp Ala Glu Asp Gln His Ser	440	445	450
Gln Gly Gly Phe	Val Val Gln Pro Pro Ala Leu Trp Gln Thr Glu			



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 <211> 739  
 <212> PRT  
 <213> Homo sapiens

<400> 86  
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 Gly Lys Lys Asp Arg Asp Ser Cys Gly Arg Lys Asn Ser Glu Pro  
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Gln	Gly	Leu	Asn	Phe	Leu	Leu	Leu	Phe	Thr	Lys	Met	Leu	Phe	Ile		50	55	60
Phe	Asn	Phe	Leu	Phe	Ser	Pro	Leu	Pro	Thr	Pro	Ala	Leu	Ile	Cys		65	70	75
Ile	Leu	Thr	Phe	Gly	Ala	Ala	Ile	Phe	Leu	Trp	Leu	Ile	Thr	Arg		80	85	90
Pro	Gln	Pro	Val	Leu	Pro	Leu	Leu	Asp	Leu	Asn	Asn	Gln	Ser	Val		95	100	105
Gly	Ile	Glu	Gly	Gly	Ala	Arg	Lys	Gly	Val	Ser	Gln	Lys	Asn	Asn		110	115	120
Asp	Leu	Thr	Ser	Cys	Cys	Phe	Ser	Asp	Ala	Lys	Thr	Met	Tyr	Glu		125	130	135
Val	Phe	Gln	Arg	Gly	Leu	Ala	Val	Ser	Asp	Asn	Gly	Pro	Cys	Leu		140	145	150
Gly	Tyr	Arg	Lys	Pro	Asn	Gln	Pro	Tyr	Arg	Trp	Leu	Ser	Tyr	Lys		155	160	165
Gln	Val	Ser	Asp	Arg	Ala	Glu	Tyr	Leu	Gly	Ser	Cys	Leu	Leu	His		170	175	180
Lys	Gly	Tyr	Lys	Ser	Ser	Pro	Asp	Gln	Phe	Val	Gly	Ile	Phe	Ala		185	190	195
Gln	Asn	Arg	Pro	Glu	Trp	Ile	Ile	Ser	Glu	Leu	Ala	Cys	Tyr	Thr		200	205	210
Tyr	Ser	Met	Val	Ala	Val	Pro	Leu	Tyr	Asp	Thr	Leu	Gly	Pro	Glu		215	220	225
Ala	Ile	Val	His	Ile	Val	Asn	Lys	Ala	Asp	Ile	Ala	Met	Val	Ile		230	235	240
Cys	Asp	Thr	Pro	Gln	Lys	Ala	Leu	Val	Leu	Ile	Gly	Asn	Val	Glu		245	250	255
Lys	Gly	Phe	Thr	Pro	Ser	Leu	Lys	Val	Ile	Ile	Leu	Met	Asp	Pro		260	265	270
Phe	Asp	Asp	Asp	Leu	Lys	Gln	Arg	Gly	Glu	Lys	Ser	Gly	Ile	Glu		275	280	285
Ile	Leu	Ser	Leu	Tyr	Asp	Ala	Glu	Asn	Leu	Gly	Lys	Glu	His	Phe		290	295	300
Arg	Lys	Pro	Val	Pro	Pro	Ser	Pro	Glu	Asp	Leu	Ser	Val	Ile	Cys		305	310	315
Phe	Thr	Ser	Gly	Thr	Thr	Gly	Asp	Pro	Lys	Gly	Ala	Met	Ile	Thr				

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His Gln Asn Ile Val Ser Asn Ala Ala	Ala Phe Leu Lys Cys Val	
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Glu His Ala Tyr Glu Pro Thr Pro Asp	Asp Val Ala Ile Ser Tyr	
350	355	360
Leu Pro Leu Ala His Met Phe Glu Arg	Ile Val Gln Ala Val Val	
365	370	375
Tyr Ser Cys Gly Ala Arg Val Gly Phe	Phe Gln Gly Asp Ile Arg	
380	385	390
Leu Leu Ala Asp Asp Met Lys Thr Leu	Lys Pro Thr Leu Phe Pro	
395	400	405
Ala Val Pro Arg Leu Leu Asn Arg Ile	Tyr Asp Lys Val Gln Asn	
410	415	420
Glu Ala Lys Thr Pro Leu Lys Lys Phe	Leu Leu Lys Leu Ala Val	
425	430	435
Ser Ser Lys Phe Lys Glu Leu Gln Lys	Gly Ile Ile Arg His Asp	
440	445	450
Ser Phe Trp Asp Lys Leu Ile Phe Ala	Lys Ile Gln Asp Ser Leu	
455	460	465
Gly Gly Arg Val Arg Val Ile Val Thr	Gly Ala Ala Pro Met Ser	
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Thr Ser Val Met Thr Phe Phe Arg Ala	Ala Met Gly Cys Gln Val	
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Tyr Glu Ala Tyr Gly Gln Thr Glu Cys	Thr Gly Gly Cys Thr Phe	
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Ala Cys Asn Tyr Val Lys Leu Glu Asp	Val Ala Asp Met Asn Tyr	
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Phe Thr Val Asn Asn Glu Gly Glu Val	Cys Ile Lys Gly Thr Asn	
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Val Phe Lys Gly Tyr Leu Lys Asp Pro	Glu Lys Thr Gln Glu Ala	
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Leu Asp Ser Asp Gly Trp Leu His Thr	Gly Asp Ile Gly Arg Trp	
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Leu Pro Asn Gly Thr Leu Lys Ile Ile	Asp Arg Lys Lys Asn Ile	
590	595	600
Phe Lys Leu Ala Gln Gly Glu Tyr Ile	Ala Pro Glu Lys Ile Glu	
605	610	615

Asn Ile Tyr Asn Arg Ser Gln Pro Val	Leu Gln Ile Phe Val His
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Gly Glu Ser Leu Arg Ser Ser Leu Val	Gly Val Val Val Pro Asp
635	640 645
Thr Asp Val Leu Pro Ser Phe Ala Ala	Lys Leu Gly Val Lys Gly
650	655 660
Ser Phe Glu Glu Leu Cys Gln Asn Gln	Val Val Arg Glu Ala Ile
665	670 675
Leu Glu Asp Leu Gln Lys Ile Gly Lys	Glu Ser Gly Leu Lys Thr
680	685 690
Phe Glu Gln Val Lys Ala Ile Phe Leu	His Pro Glu Pro Phe Ser
695	700 705
Ile Glu Asn Gly Leu Leu Thr Pro Thr	Leu Lys Ala Lys Arg Gly
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Glu Leu Ser Lys Tyr Phe Arg Thr Gln	Ile Asp Ser Leu Tyr Glu
725	730 735

His Ile Gln Asp

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 <211> 2725  
 <212> DNA  
 <213> Homo sapiens

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 <211> 660  
 <212> PRT  
 <213> Homo sapiens

<400> 88  
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                     20                    25                    30  
 Asn Gln Arg Ala Leu Arg Arg Phe Cys Gln Thr Gly Ala Val Leu  
                     35                    40                    45  
 Phe Leu Leu Val Thr Val Ile Val Asn Ile Lys Leu Ile Leu Asp  
                     50                    55                    60  
 Thr Arg Arg Ala Ile Ser Glu Ala Asn Glu Asp Pro Glu Pro Glu  
                     65                    70                    75  
 Gln Asp Tyr Asp Glu Ala Leu Gly Arg Leu Glu Pro Pro Arg Arg  
                     80                    85                    90  
 Arg Gly Ser Gly Pro Arg Arg Val Leu Asp Val Glu Val Tyr Ser  
                     95                    100                    105  
 Ser Arg Ser Lys Val Tyr Val Ala Val Asp Gly Thr Thr Val Leu  
                     110                    115                    120  
 Glu Asp Glu Ala Arg Glu Gln Gly Arg Gly Ile His Val Ile Val  
                     125                    130                    135

Leu Asn Gln Ala Thr Gly His Val Met Ala Lys Arg Val Phe Asp	140	145	150
Thr Tyr Ser Pro His Glu Asp Glu Ala Met Val Leu Phe Leu Asn	155	160	165
Met Val Ala Pro Gly Arg Val Leu Ile Cys Thr Val Lys Asp Glu	170	175	180
Gly Ser Phe His Leu Lys Asp Thr Ala Lys Ala Leu Leu Arg Ser	185	190	195
Leu Gly Ser Gln Ala Gly Pro Ala Leu Gly Trp Arg Asp Thr Trp	200	205	210
Ala Phe Val Gly Arg Lys Gly Gly Pro Val Phe Gly Glu Lys His	215	220	225
Ser Lys Ser Pro Ala Leu Ser Ser Trp Gly Asp Pro Val Leu Leu	230	235	240
Lys Thr Asp Val Pro Leu Ser Ser Ala Glu Glu Ala Glu Cys His	245	250	255
Trp Ala Asp Thr Glu Leu Asn Arg Arg Arg Arg Arg Phe Cys Ser	260	265	270
Lys Val Glu Gly Tyr Gly Ser Val Cys Ser Cys Lys Asp Pro Thr	275	280	285
Pro Ile Glu Phe Ser Pro Asp Pro Leu Pro Asp Asn Lys Val Leu	290	295	300
Asn Val Pro Val Ala Val Ile Ala Gly Asn Arg Pro Asn Tyr Leu	305	310	315
Tyr Arg Met Leu Arg Ser Leu Leu Ser Ala Gln Gly Val Ser Pro	320	325	330
Gln Met Ile Thr Val Phe Ile Asp Gly Tyr Tyr Glu Glu Pro Met	335	340	345
Asp Val Val Ala Leu Phe Gly Leu Arg Gly Ile Gln His Thr Pro	350	355	360
Ile Ser Ile Lys Asn Ala Arg Val Ser Gln His Tyr Lys Ala Ser	365	370	375
Leu Thr Ala Thr Phe Asn Leu Phe Pro Glu Ala Lys Phe Ala Val	380	385	390
Val Leu Glu Glu Asp Leu Asp Ile Ala Val Asp Phe Phe Ser Phe	395	400	405
Leu Ser Gln Ser Ile His Leu Leu Glu Glu Asp Asp Ser Leu Tyr	410	415	420
Cys Ile Ser Ala Trp Asn Asp Gln Gly Tyr Glu His Thr Ala Glu			

	425		430		435
Asp Pro Ala Leu	Leu Tyr Arg Val Glu	Thr Met Pro Gly Leu	Gly		
	440		445		450
Trp Val Leu Arg	Arg Ser Leu Tyr Lys	Glu Glu Leu Glu Pro	Lys		
	455		460		465
Trp Pro Thr Pro	Glu Lys Leu Trp Asp	Trp Asp Met Trp Met	Arg		
	470		475		480
Met Pro Glu Gln	Arg Arg Gly Arg Glu	Cys Ile Ile Pro Asp	Val		
	485		490		495
Ser Arg Ser Tyr	His Phe Gly Ile Val	Gly Leu Asn Met Asn	Gly		
	500		505		510
Tyr Phe His Glu	Ala Tyr Phe Lys Lys	His Lys Phe Asn Thr	Val		
	515		520		525
Pro Gly Val Gln	Leu Arg Asn Val Asp	Ser Leu Lys Lys Glu	Ala		
	530		535		540
Tyr Glu Val Glu	Val His Arg Leu Leu	Ser Glu Ala Glu Val	Leu		
	545		550		555
Asp His Ser Lys	Asn Pro Cys Glu Asp	Ser Phe Leu Pro Asp	Thr		
	560		565		570
Glu Gly His Thr	Tyr Val Ala Phe Ile	Arg Met Glu Lys Asp	Asp		
	575		580		585
Asp Phe Thr Thr	Trp Thr Gln Leu Ala	Lys Cys Leu His Ile	Trp		
	590		595		600
Asp Leu Asp Val	Arg Gly Asn His Arg	Gly Leu Trp Arg Leu	Phe		
	605		610		615
Arg Lys Lys Asn	His Phe Leu Val Val	Gly Val Pro Ala Ser	Pro		
	620		625		630
Tyr Ser Val Lys	Lys Pro Pro Ser Val	Thr Pro Ile Phe Leu	Glu		
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Pro Pro Pro Lys	Glu Glu Gly Ala Pro	Gly Ala Pro Glu Gln	Thr		
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<210> 89

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 89

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<210> 90  
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<212> DNA  
<213> Artificial

<220>  
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<222> 1-22  
<223> Synthetic construct.

<400> 90  
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<210> 91  
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<212> DNA  
<213> Artificial

<220>  
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<223> Synthetic construct.

<400> 91  
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<210> 92  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
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<222> 1-26  
<223> Synthetic construct.

<400> 92  
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<212> DNA  
<213> Artificial

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<400> 93  
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<210> 94  
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<400> 94

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 ggatgatttc atctccatta gcctgctgtc tctggctatg ttggtgggat 200  
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 <212> PRT  
 <213> Homo sapiens

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 Ser Glu Glu Arg Leu Lys Leu Val Thr Val Leu Gly Ala Gly Leu  
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 50 55 60  
 Ala Leu Tyr Glu Asp Ile Leu Glu Gly Lys His His Gln Ala Ser  
 65 70 75  
 Glu Thr His Asn Val Ile Ala Ser Asp Lys Ala Ala Glu Lys Ser  
 80 85 90  
 Val Val His Glu His Glu His Ser His Asp His Thr Gln Leu His  
 95 100 105  
 Ala Tyr Ile Gly Val Ser Leu Val Leu Gly Phe Val Phe Met Leu  
 110 115 120  
 Leu Val Asp Gln Ile Gly Asn Ser His Val His Ser Thr Asp Asp  
 125 130 135  
 Pro Glu Ala Ala Arg Ser Ser Asn Ser Lys Ile Thr Thr Thr Leu  
 140 145 150  
 Gly Leu Val Val His Ala Ala Ala Asp Gly Val Ala Leu Gly Ala  
 155 160 165  
 Ala Ala Ser Thr Ser Gln Thr Ser Val Gln Leu Ile Val Phe Val  
 170 175 180  
 Ala Ile Met Leu His Lys Ala Pro Ala Ala Phe Gly Leu Val Ser  
 185 190 195  
 Phe Leu Met His Ala Gly Leu Glu Arg Asn Arg Ile Arg Lys His  
 200 205 210  
 Leu Leu Val Phe Ala Leu Ala Ala Pro Val Met Ser Met Val Thr  
 215 220 225  
 Tyr Leu Gly Leu Ser Lys Ser Ser Lys Glu Ala Leu Ser Glu Val

230	235	240
Asn Ala Thr Gly Val Ala Met Leu Phe	Ser Ala Gly Thr Phe Leu	
245	250	255
Tyr Val Ala Thr Val His Val Leu Pro	Glu Val Gly Gly Ile Gly	
260	265	270
His Ser His Lys Pro Asp Ala Thr Gly	Gly Arg Gly Leu Ser Arg	
275	280	285
Leu Glu Val Ala Ala Leu Val Leu Gly	Cys Leu Ile Pro Leu Ile	
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Leu Ser Val Gly His Gln His		
305		

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<211> 25

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<213> Artificial

<220>

<221> Artificial sequence

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<223> Synthetic construct.

<400> 96

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<213> Artificial

<220>

<221> Artificial sequence

<222> 1-25

<223> Synthetic construct.

<400> 97

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<210> 98

<211> 50

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<213> Artificial

<220>

<221> Artificial sequence

<222> 1-50

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<211> 1429



<212> DNA  
<213> Homo sapiens

<400> 99

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<210> 100

<211> 401

<212> PRT

<213> Homo sapiens

<400> 100

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Asn	Tyr	Trp	Ile	Ala	Ser	Ser	Arg	Ser	Val	Asp	Leu	Gln	Thr	Arg
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Ile	Met	Glu	Leu	Glu	Gly	Arg	Val	Arg	Arg	Ala	Ala	Ala	Glu	Arg
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Gly	Ala	Val	Glu	Leu	Lys	Lys	Asn	Glu	Phe	Gln	Gly	Glu	Leu	Glu
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Lys	Gln	Arg	Glu	Gln	Leu	Asp	Lys	Ile	Gln	Ser	Ser	His	Asn	Phe
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Gln	Leu	Glu	Ser	Val	Asn	Lys	Leu	Tyr	Gln	Asp	Glu	Lys	Ala	Val
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Leu	Val	Asn	Asn	Ile	Thr	Thr	Gly	Glu	Arg	Leu	Ile	Arg	Val	Leu
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Gln	Asp	Gln	Leu	Lys	Thr	Leu	Gln	Arg	Asn	Tyr	Gly	Arg	Leu	Gln
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Gln	Asp	Val	Leu	Gln	Phe	Gln	Lys	Asn	Gln	Thr	Asn	Leu	Glu	Arg
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Lys	Phe	Ser	Tyr	Asp	Leu	Ser	Gln	Cys	Ile	Asn	Gln	Met	Lys	Glu
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Val	Lys	Glu	Gln	Cys	Glu	Glu	Arg	Ile	Glu	Glu	Val	Thr	Lys	Lys
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Gly	Asn	Glu	Ala	Val	Ala	Ser	Arg	Asp	Leu	Ser	Glu	Asn	Asn	Asp
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Gln	Arg	Gln	Gln	Leu	Gln	Ala	Leu	Ser	Glu	Pro	Gln	Pro	Arg	Leu
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Gln	Ala	Ala	Gly	Leu	Pro	His	Thr	Glu	Val	Pro	Gln	Gly	Lys	Gly
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Asn	Val	Leu	Gly	Asn	Ser	Lys	Ser	Gln	Thr	Pro	Ala	Pro	Ser	Ser
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 <212> PRT  
 <213> Homo sapiens

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 Thr Arg Leu Glu Leu Thr Asn His Ser Ser Cys Gln Glu Pro Pro  
 35 40 45  
 Gly Pro Gly Ser Leu Pro Trp Gly Ser Gln Gly Lys Pro Gly Ala  
 50 55 60  
 Cys Trp Met Ala Ser Arg Phe Ser Arg Val Val Leu Val Leu Ile  
 65 70 75  
 Asp Ala Leu Arg Phe Asp Phe Ala Gln Pro Gln His Ser His Val  
 80 85 90  
 Pro Arg Glu Pro Pro Val Ser Leu Pro Phe Leu Gly Lys Leu Ser  
 95 100 105  
 Ser Leu Gln Arg Ile Leu Glu Ile Gln Pro His His Ala Arg Leu  
 110 115 120  
 Tyr Arg Ser Gln Val Asp Pro Pro Thr Thr Thr Met Gln Arg Leu  
 125 130 135  
 Lys Ala Leu Thr Thr Gly Ser Leu Pro Thr Phe Ile Asp Ala Gly  
 140 145 150  
 Ser Asn Phe Ala Ser His Ala Ile Val Glu Asp Asn Leu Ile Lys  
 155 160 165  
 Gln Leu Thr Ser Ala Gly Arg Arg Val Val Phe Met Gly Asp Asp  
 170 175 180  
 Thr Trp Lys Asp Leu Phe Pro Gly Ala Phe Ser Lys Ala Phe Phe  
 185 190 195  
 Phe Pro Ser Phe Asn Val Arg Asp Leu Asp Thr Val Asp Asn Gly

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Ile Leu Glu His	Leu Tyr Pro Thr Met	Asp Ser Gly Glu Trp	Asp
	215	220	225
Val Leu Ile Ala	His Phe Leu Gly Val	Asp His Cys Gly His	Lys
	230	235	240
His Gly Pro His	His Pro Glu Met Ala	Lys Lys Leu Ser Gln	Met
	245	250	255
Asp Gln Val Ile	Gln Gly Leu Val Glu	Arg Leu Glu Asn Asp	Thr
	260	265	270
Leu Leu Val Val	Ala Gly Asp His Gly	Met Thr Thr Asn Gly	Asp
	275	280	285
His Gly Gly Asp	Ser Glu Leu Glu Val	Ser Ala Ala Leu Phe	Leu
	290	295	300
Tyr Ser Pro Thr	Ala Val Phe Pro Ser	Thr Pro Pro Glu Glu	Pro
	305	310	315
Glu Val Ile Pro	Gln Val Ser Leu Val	Pro Thr Leu Ala Leu	Leu
	320	325	330
Leu Gly Leu Pro	Ile Pro Phe Gly Asn	Ile Gly Glu Val Met	Ala
	335	340	345
Glu Leu Phe Ser	Gly Gly Glu Asp Ser	Gln Pro His Ser Ser	Ala
	350	355	360
Leu Ala Gln Ala	Ser Ala Leu His Leu	Asn Ala Gln Gln Val	Ser
	365	370	375
Arg Phe Leu His	Thr Tyr Ser Ala Ala	Thr Gln Asp Leu Gln	Ala
	380	385	390
Lys Glu Leu His	Gln Leu Gln Asn Leu	Phe Ser Lys Ala Ser	Ala
	395	400	405
Asp Tyr Gln Trp	Leu Leu Gln Ser Pro	Lys Gly Ala Glu Ala	Thr
	410	415	420
Leu Pro Thr Val	Ile Ala Glu Leu Gln	Gln Phe Leu Arg Gly	Ala
	425	430	435
Arg Ala Met Cys	Ile Glu Ser Trp Ala	Arg Phe Ser Leu Val	Arg
	440	445	450
Met Ala Gly Gly	Thr Ala Leu Leu Ala	Ala Ser Cys Phe Ile	Cys
	455	460	465
Leu Leu Ala Ser	Gln Trp Ala Ile Ser	Pro Gly Phe Pro Phe	Cys
	470	475	480
Pro Leu Leu Leu	Thr Pro Val Ala Trp	Gly Leu Val Gly Ala	Ile
	485	490	495

Ala Tyr Ala Gly	Leu Leu Gly Thr Ile	Glu Leu Lys Leu Asp	Leu
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Val Leu Leu Gly	Ala Val Ala Ala Val	Ser Ser Phe Leu Pro	Phe
515	520		525
Leu Trp Lys Ala	Trp Ala Gly Trp Gly	Ser Lys Arg Pro Leu	Ala
530	535		540
Thr Leu Phe Pro	Ile Pro Gly Pro Val	Leu Leu Leu Leu Leu	Phe
545	550		555
Arg Leu Ala Val	Phe Phe Ser Asp Ser	Phe Val Val Ala Glu	Ala
560	565		570
Arg Ala Thr Pro	Phe Leu Leu Gly Ser	Phe Ile Leu Leu Leu	Val
575	580		585
Val Gln Leu His	Trp Glu Gly Gln Leu	Leu Pro Pro Lys Leu	Leu
590	595		600
Thr Met Pro Arg	Leu Gly Thr Ser Ala	Thr Thr Asn Pro Pro	Arg
605	610		615
His Asn Gly Ala	Tyr Ala Leu Arg Leu	Gly Ile Gly Leu Leu	Leu
620	625		630
Cys Thr Arg Leu	Ala Gly Leu Phe His	Arg Cys Pro Glu Glu	Thr
635	640		645
Pro Val Cys His	Ser Ser Pro Trp Leu	Ser Pro Leu Ala Ser	Met
650	655		660
Val Gly Gly Arg	Ala Lys Asn Leu Trp	Tyr Gly Ala Cys Val	Ala
665	670		675
Ala Leu Val Ala	Leu Leu Ala Ala Val	Arg Leu Trp Leu Arg	Arg
680	685		690
Tyr Gly Asn Leu	Lys Ser Pro Glu Pro	Pro Met Leu Phe Val	Arg
695	700		705
Trp Gly Leu Pro	Leu Met Ala Leu Gly	Thr Ala Ala Tyr Trp	Ala
710	715		720
Leu Ala Ser Gly	Ala Asp Glu Ala Pro	Pro Arg Leu Arg Val	Leu
725	730		735
Val Ser Gly Ala	Ser Met Val Leu Pro	Arg Ala Val Ala Gly	Leu
740	745		750
Ala Ala Ser Gly	Leu Ala Leu Leu Leu	Trp Lys Pro Val Thr	Val
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Leu Val Lys Ala	Gly Ala Gly Ala Pro	Arg Thr Arg Thr Val	Leu
770	775		780
Thr Pro Phe Ser	Gly Pro Pro Thr Ser	Gln Ala Asp Leu Asp	Tyr



785	790	795
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Arg Leu Glu Arg Thr Lys Ser Gln Gly	Pro Leu Thr Val Ala Ala	
815	820	825
Tyr Gln Leu Gly Ser Val Tyr Ser Ala	Ala Met Val Thr Ala Leu	
830	835	840
Thr Leu Leu Ala Phe Pro Leu Leu Leu	Leu His Ala Glu Arg Ile	
845	850	855
Ser Leu Val Phe Leu Leu Leu Phe Leu	Gln Ser Phe Leu Leu Leu	
860	865	870
His Leu Leu Ala Ala Gly Ile Pro Val	Thr Thr Pro Gly Pro Phe	
875	880	885
Thr Val Pro Trp Gln Ala Val Ser Ala	Trp Ala Leu Met Ala Thr	
890	895	900
Gln Thr Phe Tyr Ser Thr Gly His Gln	Pro Val Phe Pro Ala Ile	
905	910	915
His Trp His Ala Ala Phe Val Gly Phe	Pro Glu Gly His Gly Ser	
920	925	930
Cys Thr Trp Leu Pro Ala Leu Leu Val	Gly Ala Asn Thr Phe Ala	
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Ser His Leu Leu Phe Ala Val Gly Cys	Pro Leu Leu Leu Leu Trp	
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Pro Phe Leu Cys Glu Ser Gln Gly Leu	Arg Lys Arg Gln Gln Pro	
965	970	975
Pro Gly Asn Glu Ala Asp Ala Arg Val	Arg Pro Glu Glu Glu Glu	
980	985	990
Glu Pro Leu Met Glu Met Arg Leu Arg	Asp Ala Pro Gln His Phe	
995	1000	1005
Tyr Ala Ala Leu Leu Gln Leu Gly Leu	Lys Tyr Leu Phe Ile Leu	
1010	1015	1020
Gly Ile Gln Ile Leu Ala Cys Ala Leu	Ala Ala Ser Ile Leu Arg	
1025	1030	1035
Arg His Leu Met Val Trp Lys Val Phe	Ala Pro Lys Phe Ile Phe	
1040	1045	1050
Glu Ala Val Gly Phe Ile Val Ser Ser	Val Gly Leu Leu Leu Gly	
1055	1060	1065
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Arg Gln Leu Phe Leu Ala Gln Gln Arg  
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gaggaagagc catcgacgac cctggctcgc tgggatcccc aaactggcag 1250

gctgtgtatt ccttcgctgt ccagcttcga ccaggattca gagggctgcg 1300  
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<210> 104

<211> 442

<212> PRT

<213> Homo sapiens

<400> 104

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Leu	Leu	Thr	Leu	Cys	Ser	Ile	Ser	Ser	Gln	Ile	Gly	Pro	Pro	Glu
				20					25					30
Val	Ala	Leu	Thr	Thr	Asp	Glu	Lys	Ser	Ile	Ser	Val	Val	Leu	Thr
				35					40					45
Ala	Pro	Glu	Lys	Trp	Lys	Arg	Asn	Pro	Glu	Asp	Leu	Pro	Val	Ser
				50					55					60
Met	Gln	Gln	Ile	Tyr	Ser	Asn	Leu	Lys	Tyr	Asn	Val	Ser	Val	Leu
				65					70					75
Asn	Thr	Lys	Ser	Asn	Arg	Thr	Trp	Ser	Gln	Cys	Val	Thr	Asn	His
				80					85					90
Thr	Leu	Val	Leu	Thr	Trp	Leu	Glu	Pro	Asn	Thr	Leu	Tyr	Cys	Val
				95					100					105
His	Val	Glu	Ser	Phe	Val	Pro	Gly	Pro	Pro	Arg	Arg	Ala	Gln	Pro
				110					115					120
Ser	Glu	Lys	Gln	Cys	Ala	Arg	Thr	Leu	Lys	Asp	Gln	Ser	Ser	Glu
				125					130					135
Phe	Lys	Ala	Lys	Ile	Ile	Phe	Trp	Tyr	Val	Leu	Pro	Ile	Ser	Ile
				140					145					150
Thr	Val	Phe	Leu	Phe	Ser	Val	Met	Gly	Tyr	Ser	Ile	Tyr	Arg	Tyr
				155					160					165

Ile	His	Val	Gly	Lys	Glu	Lys	His	Pro	Ala	Asn	Leu	Ile	Leu	Ile	
				170					175					180	
Tyr	Gly	Asn	Glu	Phe	Asp	Lys	Arg	Phe	Phe	Val	Pro	Ala	Glu	Lys	
				185					190					195	
Ile	Val	Ile	Asn	Phe	Ile	Thr	Leu	Asn	Ile	Ser	Asp	Asp	Ser	Lys	
				200					205					210	
Ile	Ser	His	Gln	Asp	Met	Ser	Leu	Leu	Gly	Lys	Ser	Ser	Asp	Val	
				215					220					225	
Ser	Ser	Leu	Asn	Asp	Pro	Gln	Pro	Ser	Gly	Asn	Leu	Arg	Pro	Pro	
				230					235					240	
Gln	Glu	Glu	Glu	Glu	Val	Lys	His	Leu	Gly	Tyr	Ala	Ser	His	Leu	
				245					250					255	
Met	Glu	Ile	Phe	Cys	Asp	Ser	Glu	Glu	Asn	Thr	Glu	Gly	Thr	Ser	
				260					265					270	
Leu	Thr	Gln	Gln	Glu	Ser	Leu	Ser	Arg	Thr	Ile	Pro	Pro	Asp	Lys	
				275					280					285	
Thr	Val	Ile	Glu	Tyr	Glu	Tyr	Asp	Val	Arg	Thr	Thr	Asp	Ile	Cys	
				290					295					300	
Ala	Gly	Pro	Glu	Glu	Gln	Glu	Leu	Ser	Leu	Gln	Glu	Glu	Val	Ser	
				305					310					315	
Thr	Gln	Gly	Thr	Leu	Leu	Glu	Ser	Gln	Ala	Ala	Leu	Ala	Val	Leu	
				320					325					330	
Gly	Pro	Gln	Thr	Leu	Gln	Tyr	Ser	Tyr	Thr	Pro	Gln	Leu	Gln	Asp	
				335					340					345	
Leu	Asp	Pro	Leu	Ala	Gln	Glu	His	Thr	Asp	Ser	Glu	Glu	Gly	Pro	
				350					355					360	
Glu	Glu	Glu	Pro	Ser	Thr	Thr	Leu	Val	Asp	Trp	Asp	Pro	Gln	Thr	
				365					370					375	
Gly	Arg	Leu	Cys	Ile	Pro	Ser	Leu	Ser	Ser	Phe	Asp	Gln	Asp	Ser	
				380					385					390	
Glu	Gly	Cys	Glu	Pro	Ser	Glu	Gly	Asp	Gly	Leu	Gly	Glu	Glu	Gly	
				395					400					405	
Leu	Leu	Ser	Arg	Leu	Tyr	Glu	Glu	Pro	Ala	Pro	Asp	Arg	Pro	Pro	
				410					415					420	
Gly	Glu	Asn	Glu	Thr	Tyr	Leu	Met	Gln	Phe	Met	Glu	Glu	Trp	Gly	
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Leu	Tyr	Val	Gln	Met	Glu	Asn									
				440											

<210> 105

<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct

<400> 105  
cgctgctgct gttgctcctg g 21

<210> 106  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 106  
cagtgtgccca ggactttg 18

<210> 107  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 107  
agtcgcaggc agcgttgg 18

<210> 108  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 108  
ctcctccgag tctgtgtgct cctgc 25

<210> 109  
<211> 51  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence

<222> 1-51  
<223> Synthetic construct.

<400> 109  
ggacgggcag ttccctgtgt ctctgggtggg ttgcctaaac ctgcaaacaat 50  
c 51

<210> 110  
<211> 1114  
<212> DNA  
<213> Homo sapiens

<400> 110  
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tctgtgact gtggccaccg ccctgatgct gcccgtaag cccccgcag 150  
gctcctgggg ggcccagatc atcgggggcc acgaggtgac cccccactcc 200  
aggccctaca tggcatccgt gcgcttcggg ggccaacatc actgcggagg 250  
cttcctgctg cgagcccgct ggggtggtctc ggccgcccac tgcttcagcc 300  
acagagacct ccgcactggc ctggtggtgc tgggcgcca cgtcctgagt 350  
actgcggagc ccaccagca ggtgtttggc atcgatgctc tcaccacgca 400  
ccccgactac caccocatga cccacgcaa cgacatctgc ctgctgcggc 450  
tgaacggctc tgctgtcctg ggccctgcag tggggctgct gaggtgcc 500  
gggagaaggg ccaggcccc cacagcggg acacggtgcc ggggtggctgg 550  
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cacctgacac ttaccatgct ctgcaccgc agtggggaca gccacagacg 700  
gggcttctgc tcggccgact ccggagggcc cctggtgtgc aggaaccggg 750  
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gccgtccag gcctggaatg ttccgtggct gggccccacg ggaagcctga 1000  
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aaaaaaaaa gaaa 1114

<210> 111

<211> 283

<212> PRT

<213> Homo sapiens

<400> 111

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Ala	Thr	Ala	Leu	Met	Leu	Pro	Val	Lys	Pro	Pro	Ala	Gly	Ser	Trp
				20					25					30

Gly	Ala	Gln	Ile	Ile	Gly	Gly	His	Glu	Val	Thr	Pro	His	Ser	Arg
			35						40					45

Pro	Tyr	Met	Ala	Ser	Val	Arg	Phe	Gly	Gly	Gln	His	His	Cys	Gly
				50					55					60

Gly	Phe	Leu	Leu	Arg	Ala	Arg	Trp	Val	Val	Ser	Ala	Ala	His	Cys
				65					70					75

Phe	Ser	His	Arg	Asp	Leu	Arg	Thr	Gly	Leu	Val	Val	Leu	Gly	Ala
				80					85					90

His	Val	Leu	Ser	Thr	Ala	Glu	Pro	Thr	Gln	Gln	Val	Phe	Gly	Ile
				95					100					105

Asp	Ala	Leu	Thr	Thr	His	Pro	Asp	Tyr	His	Pro	Met	Thr	His	Ala
				110					115					120

Asn	Asp	Ile	Cys	Leu	Leu	Arg	Leu	Asn	Gly	Ser	Ala	Val	Leu	Gly
				125					130					135

Pro	Ala	Val	Gly	Leu	Leu	Arg	Leu	Pro	Gly	Arg	Arg	Ala	Arg	Pro
				140					145					150

Pro	Thr	Ala	Gly	Thr	Arg	Cys	Arg	Val	Ala	Gly	Trp	Gly	Phe	Val
				155					160					165

Ser	Asp	Phe	Glu	Glu	Leu	Pro	Pro	Gly	Leu	Met	Glu	Ala	Lys	Val
				170					175					180

Arg	Val	Leu	Asp	Pro	Asp	Val	Cys	Asn	Ser	Ser	Trp	Lys	Gly	His
				185					190					195

Leu	Thr	Leu	Thr	Met	Leu	Cys	Thr	Arg	Ser	Gly	Asp	Ser	His	Arg
				200					205					210

Arg	Gly	Phe	Cys	Ser	Ala	Asp	Ser	Gly	Gly	Pro	Leu	Val	Cys	Arg
				215					220					225

Asn	Arg	Ala	His	Gly	Leu	Val	Ser	Phe	Ser	Gly	Leu	Trp	Cys	Gly
				230					235					240

Asp	Pro	Lys	Thr	Pro	Asp	Val	Tyr	Thr	Gln	Val	Ser	Ala	Phe	Val
				245					250					255

Ala Trp Ile Trp Asp Val Val Arg Arg Ser Ser Pro Gln Pro Gly  
 260 265 270

Pro Leu Pro Gly Thr Thr Arg Pro Pro Gly Glu Ala Ala  
 275 280

<210> 112  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 112  
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<210> 113  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 113  
 cgagaaggaa acgaggccgt gag 23

<210> 114  
 <211> 44  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-44  
 <223> Synthetic construct.

<400> 114  
 tgacacttac catgctctgc acccgcagtg gggacagcca caga 44

<210> 115  
 <211> 1808  
 <212> DNA  
 <213> Homo sapiens

<400> 115  
 gagctaccca ggcggctggt gtgcagcaag ctccgcgcg actccggacg 50  
 cctgacgcct gacgcctgtc cccggcccgg catgagccgc tacctgctgc 100  
 cgctgtcggc gctgggcacg gtagcaggcg ccgccgtgct gctcaaggac 150  
 tatgtcaccc gtggggcttg cccagcaag gccaccatcc ctgggaagac 200



ggtcatcgtg acggg'gccca acacaggcat cggaagcag accgccttgg 250  
 aactggccag gagaggaggc aacatcatcc tggcctgccg agacatggag 300  
 aagtgtgagg cggcagcaaa ggacatccgc ggggagaccc tcaatcacca 350  
 tgtcaacgcc cggcacctgg acttggttc cctcaagtct atccgagagt 400  
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 aacgcgggtg tgatgcgggtg cccccactgg accaccgagg acggcttcga 500  
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 gcctgtcggg gagggttcca aggtgctccg tgaagagcat gggcaagttg 1450  
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 gtccctctctg agccttggtt tcttcagcag tgagatgctc agaataactg 1550  
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gagagcaggt gcaggtgtca tcccgagttc aggctctgca cggcatggag 1700  
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 gctcattt 1808

<210> 116  
 <211> 331  
 <212> PRT  
 <213> Homo sapiens

<400> 116  
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 Gly Ala Ala Val Leu Leu Lys Asp Tyr Val Thr Gly Gly Ala Cys  
 20 25 30  
 Pro Ser Lys Ala Thr Ile Pro Gly Lys Thr Val Ile Val Thr Gly  
 35 40 45  
 Ala Asn Thr Gly Ile Gly Lys Gln Thr Ala Leu Glu Leu Ala Arg  
 50 55 60  
 Arg Gly Gly Asn Ile Ile Leu Ala Cys Arg Asp Met Glu Lys Cys  
 65 70 75  
 Glu Ala Ala Ala Lys Asp Ile Arg Gly Glu Thr Leu Asn His His  
 80 85 90  
 Val Asn Ala Arg His Leu Asp Leu Ala Ser Leu Lys Ser Ile Arg  
 95 100 105  
 Glu Phe Ala Ala Lys Ile Ile Glu Glu Glu Glu Arg Val Asp Ile  
 110 115 120  
 Leu Ile Asn Asn Ala Gly Val Met Arg Cys Pro His Trp Thr Thr  
 125 130 135  
 Glu Asp Gly Phe Glu Met Gln Phe Gly Val Asn His Leu Gly His  
 140 145 150  
 Phe Leu Leu Thr Asn Leu Leu Leu Asp Lys Leu Lys Ala Ser Ala  
 155 160 165  
 Pro Ser Arg Ile Ile Asn Leu Ser Ser Leu Ala His Val Ala Gly  
 170 175 180  
 His Ile Asp Phe Asp Asp Leu Asn Trp Gln Thr Arg Lys Tyr Asn  
 185 190 195  
 Thr Lys Ala Ala Tyr Cys Gln Ser Lys Leu Ala Ile Val Leu Phe  
 200 205 210  
 Thr Lys Glu Leu Ser Arg Arg Leu Gln Gly Ser Gly Val Thr Val  
 215 220 225

Asn	Ala	Leu	His	Pro	Gly	Val	Ala	Arg	Thr	Glu	Leu	Gly	Arg	His
				230					235					240
Thr	Gly	Ile	His	Gly	Ser	Thr	Phe	Ser	Ser	Thr	Thr	Leu	Gly	Pro
				245					250					255
Ile	Phe	Trp	Leu	Leu	Val	Lys	Ser	Pro	Glu	Leu	Ala	Ala	Gln	Pro
				260					265					270
Ser	Thr	Tyr	Leu	Ala	Val	Ala	Glu	Glu	Leu	Ala	Asp	Val	Ser	Gly
				275					280					285
Lys	Tyr	Phe	Asp	Gly	Leu	Lys	Gln	Lys	Ala	Pro	Ala	Pro	Glu	Ala
				290					295					300
Glu	Asp	Glu	Glu	Val	Ala	Arg	Arg	Leu	Trp	Ala	Glu	Ser	Ala	Arg
				305					310					315
Leu	Val	Gly	Leu	Glu	Ala	Pro	Ser	Val	Arg	Glu	Gln	Pro	Leu	Pro
				320					325					330

Arg

<210> 117  
 <211> 2249  
 <212> DNA  
 <213> Homo sapiens

<400> 117  
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 gggcgacacg ttctcggcgc tgaccagcgt ggcgcgcgcc ctggcgccccg 150  
 agcgccgggt gctggggctg ctgaggcgtt acctgcgcgg ggaggaggcg 200  
 cggctgoggg acctgactag attctacgac aaggtaactt ctttgcata 250  
 ggattcaaca acccctgtgg ctaaccctct gcttgcatct acttcatca 300  
 aacgcctgca gtctgactgg aggaatgtgg tacatagtct ggaggccagt 350  
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 acctgcagac cagagacacc tacgaggggc tatgtcagac cctgggttcc 950  
 cagcccactc tctaccagat ccctagcctc tactgttctt atgagaccaa 1000  
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 agccacggaa gtcagagtag gatgcacagt acaaaggagg ggggagtggg 1900  
 ggctgagag ggaagtttct ggagttcaga tactctctgt tgggaacagg 1950  
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 cttgaccaca gggaccaaga agtggcaatg aggacacctg caggaggggc 2050  
 tagcctgact ccagaactt taagactttc tccccactgc cttctgctgc 2100  
 agccaagca gggagtgtcc ccctcccaga agcatatccc agatgagtgg 2150

tacattatat aaggattttt tttaagttga aaacaacttt cttttctttt 2200

tgtatgatgg ttttttaaca cagtcattaa aaatgtttat aaatcaaaa 2249

<210> 118

<211> 544

<212> PRT

<213> Homo sapiens

<400> 118

Met	Gly	Pro	Gly	Ala	Arg	Leu	Ala	Ala	Leu	Leu	Ala	Val	Leu	Ala
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Leu	Gly	Thr	Gly	Asp	Pro	Glu	Arg	Ala	Ala	Ala	Arg	Gly	Asp	Thr
				20					25					30

Phe	Ser	Ala	Leu	Thr	Ser	Val	Ala	Arg	Ala	Leu	Ala	Pro	Glu	Arg
				35					40					45

Arg	Leu	Leu	Gly	Leu	Leu	Arg	Arg	Tyr	Leu	Arg	Gly	Glu	Glu	Ala
				50					55					60

Arg	Leu	Arg	Asp	Leu	Thr	Arg	Phe	Tyr	Asp	Lys	Val	Leu	Ser	Leu
				65					70					75

His	Glu	Asp	Ser	Thr	Thr	Pro	Val	Ala	Asn	Pro	Leu	Leu	Ala	Phe
				80					85					90

Thr	Leu	Ile	Lys	Arg	Leu	Gln	Ser	Asp	Trp	Arg	Asn	Val	Val	His
				95					100					105

Ser	Leu	Glu	Ala	Ser	Glu	Asn	Ile	Arg	Ala	Leu	Lys	Asp	Gly	Tyr
				110					115					120

Glu	Lys	Val	Glu	Gln	Asp	Leu	Pro	Ala	Phe	Glu	Asp	Leu	Glu	Gly
				125					130					135

Ala	Ala	Arg	Ala	Leu	Met	Arg	Leu	Gln	Asp	Val	Tyr	Met	Leu	Asn
				140					145					150

Val	Lys	Gly	Leu	Ala	Arg	Gly	Val	Phe	Gln	Arg	Val	Thr	Gly	Ser
				155					160					165

Ala	Ile	Thr	Asp	Leu	Tyr	Ser	Pro	Lys	Arg	Leu	Phe	Ser	Leu	Thr
				170					175					180

Gly	Asp	Asp	Cys	Phe	Gln	Val	Gly	Lys	Val	Ala	Tyr	Asp	Met	Gly
				185					190					195

Asp	Tyr	Tyr	His	Ala	Ile	Pro	Trp	Leu	Glu	Glu	Ala	Val	Ser	Leu
				200					205					210

Phe	Arg	Gly	Ser	Tyr	Gly	Glu	Trp	Lys	Thr	Glu	Asp	Glu	Ala	Ser
				215					220					225

Leu	Glu	Asp	Ala	Leu	Asp	His	Leu	Ala	Phe	Ala	Tyr	Phe	Arg	Ala
				230					235					240

Gly	Asn	Val	Ser	Cys	Ala	Leu	Ser	Leu	Ser	Arg	Glu	Phe	Leu	Leu	
				245					250					255	
Tyr	Ser	Pro	Asp	Asn	Lys	Arg	Met	Ala	Arg	Asn	Val	Leu	Lys	Tyr	
				260					265					270	
Glu	Arg	Leu	Leu	Ala	Glu	Ser	Pro	Asn	His	Val	Val	Ala	Glu	Ala	
				275					280					285	
Val	Ile	Gln	Arg	Pro	Asn	Ile	Pro	His	Leu	Gln	Thr	Arg	Asp	Thr	
				290					295					300	
Tyr	Glu	Gly	Leu	Cys	Gln	Thr	Leu	Gly	Ser	Gln	Pro	Thr	Leu	Tyr	
				305					310					315	
Gln	Ile	Pro	Ser	Leu	Tyr	Cys	Ser	Tyr	Glu	Thr	Asn	Ser	Asn	Ala	
				320					325					330	
Tyr	Leu	Leu	Leu	Gln	Pro	Ile	Arg	Lys	Glu	Val	Ile	His	Leu	Glu	
				335					340					345	
Pro	Tyr	Ile	Ala	Leu	Tyr	His	Asp	Phe	Val	Ser	Asp	Ser	Glu	Ala	
				350					355					360	
Gln	Lys	Ile	Arg	Glu	Leu	Ala	Glu	Pro	Trp	Leu	Gln	Arg	Ser	Val	
				365					370					375	
Val	Ala	Ser	Gly	Glu	Lys	Gln	Leu	Gln	Val	Glu	Tyr	Arg	Ile	Ser	
				380					385					390	
Lys	Ser	Ala	Trp	Leu	Lys	Asp	Thr	Val	Asp	Pro	Lys	Leu	Val	Thr	
				395					400					405	
Leu	Asn	His	Arg	Ile	Ala	Ala	Leu	Thr	Gly	Leu	Asp	Val	Arg	Pro	
				410					415					420	
Pro	Tyr	Ala	Glu	Tyr	Leu	Gln	Val	Val	Asn	Tyr	Gly	Ile	Gly	Gly	
				425					430					435	
His	Tyr	Glu	Pro	His	Phe	Asp	His	Ala	Thr	Ser	Pro	Ser	Ser	Pro	
				440					445					450	
Leu	Tyr	Arg	Met	Lys	Ser	Gly	Asn	Arg	Val	Ala	Thr	Phe	Met	Ile	
				455					460					465	
Tyr	Leu	Ser	Ser	Val	Glu	Ala	Gly	Gly	Ala	Thr	Ala	Phe	Ile	Tyr	
				470					475					480	
Ala	Asn	Leu	Ser	Val	Pro	Val	Val	Arg	Asn	Ala	Ala	Leu	Phe	Trp	
				485					490					495	
Trp	Asn	Leu	His	Arg	Ser	Gly	Glu	Gly	Asp	Ser	Asp	Thr	Leu	His	
				500					505					510	
Ala	Gly	Cys	Pro	Val	Leu	Val	Gly	Asp	Lys	Trp	Val	Ala	Asn	Lys	
				515					520					525	
Trp	Ile	His	Glu	Tyr	Gly	Gln	Glu	Phe	Arg	Arg	Pro	Cys	Ser	Ser	

Ser Pro Glu Asp

<210> 119  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 119  
cgggacagga gaccagaaa ggg 23

<210> 120  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 120  
ggccaagtga tccaaggcat cttc 24

<210> 121  
<211> 49  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-49  
<223> Synthetic construct.

<400> 121  
ctgcgggacc tgactagatt ctacgacaag gtactttcctt tgcattgggg 49

<210> 122  
<211> 1778  
<212> DNA  
<213> Homo sapiens

<400> 122  
gagatagggg gtctgggttt aagttcctgc tccatctcag gagcccctgc 50  
tcccaccctt aggaagccac cagactccac ggtgtggggc caatcaggtg 100  
gaatcggccc tggcaggtgg ggccacgagc gctggctgag ggaccgagcc 150  
ggagagcccc ggagcccccg taaccgcgc ggggagcgcc caggatgccg 200

cgcggggact cggagcaggt gcgctactgc gcgcgcttct cctacctctg 250  
 gctcaagttt tcacttatca tctattccac cgtgttctgg ctgattgggg 300  
 ccctggctct gtctgtgggc atctatgcag aggttgagcg gcagaaatat 350  
 aaaacccttg aaagtgcctt cctggctcca gccatcatcc tcctcctcct 400  
 gggcgctcgt atgttcatgg tctccttcat tgggtgtgctg gcgtccctcc 450  
 gtgacaacct gtaccttctc caagcattca tgtacatcct tgggatctgc 500  
 ctcatcatgg agctcattgg tggcgtgggtg gccttgacct tccggaacca 550  
 gaccattgac ttctgaacg acaacattcg aagaggaatt gagaactact 600  
 atgatgatct ggacttcaaa aacatcatgg actttgttca gaaaaagttc 650  
 aagtgtgtg gcggggagga ctaccgagat tggagcaaga atcagtacca 700  
 cgactgcagt gcccctggac ccctggcctg tggggtgcc tacacctgct 750  
 gcatacaggaa caogacagaa gttgtcaaca ccatgtgtgg ctacaaaact 800  
 atcgacaagg agcgtttcag tgtgcaggat gtcactctac tgccgggctg 850  
 caccaacgcc gtgatcatct ggttcatgga caactacacc atcatggcgt 900  
 gcatacctct gggcatacctg cttccccagt tcctgggggt gctgctgacg 950  
 ctgctgtaca tcaccgggt ggaggacatc atcatggagc actctgtcac 1000  
 tgatgggctc ctggggcccg gtgccaagcc cagcgtggag gcggcaggca 1050  
 cgggatgctg cttgtgttac cccaattagg gccagcctg ccatggcagc 1100  
 tccaacaagg accgtctggg atagcacctc tcagtcaaca tcgtggggct 1150  
 ggacagggt gcggccctc tgcccacact cagtactgac caaagccagg 1200  
 gctgtgtgtg cctgtgtgta ggtcccacgg cctctgcctc cccagggagc 1250  
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 gtgcccacct ggggcctggg gaacaaggcc ctctttctc caggcctggg 1350  
 ctacagggga gggagagcct gaggtctctg tcagggccca tttcatctct 1400  
 ggagtgctt tggcgtgggt attcaaggca gttttgtagc acctgtaatt 1450  
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 gggcaggagg gaagagctgt ccatgcagcc acgcccattg ccaggttggc 1550  
 ctcttctcag cctcccaggt gccttgagcc ctcttgcaag ggcggtgct 1600  
 tccttgagcc tagttttttt ttacgtgatt tttgtaacat tcattttttt 1650



gtacagataa caggagtttc tgactaatca aagctggtat ttccccgcat 1700  
 gtcttattct tgcccttccc ccaaccagtt tgttaatcaa acaataaaaa 1750  
 catgttttgt tttgttttta aaaaaaaa 1778

<210> 123  
 <211> 294  
 <212> PRT  
 <213> Homo sapiens

<400> 123  
 Met Pro Arg Gly Asp Ser Glu Gln Val Arg Tyr Cys Ala Arg Phe  
 1 5 10 15  
 Ser Tyr Leu Trp Leu Lys Phe Ser Leu Ile Ile Tyr Ser Thr Val  
 20 25 30  
 Phe Trp Leu Ile Gly Ala Leu Val Leu Ser Val Gly Ile Tyr Ala  
 35 40 45  
 Glu Val Glu Arg Gln Lys Tyr Lys Thr Leu Glu Ser Ala Phe Leu  
 50 55 60  
 Ala Pro Ala Ile Ile Leu Ile Leu Leu Gly Val Val Met Phe Met  
 65 70 75  
 Val Ser Phe Ile Gly Val Leu Ala Ser Leu Arg Asp Asn Leu Tyr  
 80 85 90  
 Leu Leu Gln Ala Phe Met Tyr Ile Leu Gly Ile Cys Leu Ile Met  
 95 100 105  
 Glu Leu Ile Gly Gly Val Val Ala Leu Thr Phe Arg Asn Gln Thr  
 110 115 120  
 Ile Asp Phe Leu Asn Asp Asn Ile Arg Arg Gly Ile Glu Asn Tyr  
 125 130 135  
 Tyr Asp Asp Leu Asp Phe Lys Asn Ile Met Asp Phe Val Gln Lys  
 140 145 150  
 Lys Phe Lys Cys Cys Gly Gly Glu Asp Tyr Arg Asp Trp Ser Lys  
 155 160 165  
 Asn Gln Tyr His Asp Cys Ser Ala Pro Gly Pro Leu Ala Cys Gly  
 170 175 180  
 Val Pro Tyr Thr Cys Cys Ile Arg Asn Thr Thr Glu Val Val Asn  
 185 190 195  
 Thr Met Cys Gly Tyr Lys Thr Ile Asp Lys Glu Arg Phe Ser Val  
 200 205 210  
 Gln Asp Val Ile Tyr Val Arg Gly Cys Thr Asn Ala Val Ile Ile  
 215 220 225  
 Trp Phe Met Asp Asn Tyr Thr Ile Met Ala Cys Ile Leu Leu Gly

230	235	240
Ile Leu Leu Pro Gln Phe Leu Gly Val	Leu Leu Thr Leu Leu Tyr	
245	250	255
Ile Thr Arg Val Glu Asp Ile Ile Met	Glu His Ser Val Thr Asp	
260	265	270
Gly Leu Leu Gly Pro Gly Ala Lys Pro	Ser Val Glu Ala Ala Gly	
275	280	285
Thr Gly Cys Cys Leu Cys Tyr Pro Asn		
290		

<210> 124  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 124  
 atcatctatt ccaccgtgtt ctggc 25

<210> 125  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 125  
 gacagagtgc tccatgatga tgtoc 25

<210> 126  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 126  
 cctgtctgtg ggcatttatg cagagggtga gcggcagaaa tataaaaccc 50

<210> 127  
 <211> 1636  
 <212> DNA  
 <213> Homo sapiens

<400> 127

gaggagcggg ccgaggactc cagcgtgccc aggtctggca tcctgcactt 50  
gctgccctct gacacctggg aagatggccg gcccgaggac cttcaccctt 100  
ctctgtggtt tgctggcagc caccttgatc caagccaccc tcagtcccac 150  
tgcagttctc atcctcggcc caaaagtcac caaagaaaag ctgacacagg 200  
agctgaagga ccacaacgcc accagcatcc tgcagcagct gccgctgctc 250  
agtgccatgc gggaaaagcc agccggaggc atccctgtgc tgggcagcct 300  
ggtgaacacc gtccctgaagc acatcatctg gctgaaggct atcacagcta 350  
acatcctcca gctgcagggtg aagccctcgg ccaatgacca ggagctgcta 400  
gtcaagatcc ccctggacat ggtggctgga ttcaacacgc ccctggtcaa 450  
gaccatcgtg gagttccaca tgacgactga ggccaagcc accatccgca 500  
tggacaccag tgcaagtggc cccaccgcgc tggtcctcag tgactgtgcc 550  
accagccatg ggagcctgcg catccaactg ctgtataagc tctccttcc 600  
ggtgaacgcc ttagctaagc aggtcatgaa cctcctagt ccatccctgc 650  
ccaatctagt gaaaaaccag ctgtgtcccg tgatcgaggc ttccttcaat 700  
ggcatgtatg cagacctcct gcagctggtg aaggtgcca tttccctcag 750  
cattgaccgt ctggagtttg accttctgta tcctgccatc aagggtgaca 800  
ccattcagct ctacctgggg gccaaagtgt tggactcaca gggaaagggt 850  
accaagtggg tcaataactc tgcagcttcc ctgacaatgc ccaccctgga 900  
caacatcccg ttcagcctca tcgtgagtcg ggacgtggtg aaagctgcag 950  
tggctgctgt gctctctcca gaagaattca tggctcctgtt ggactctgtg 1000  
cttcctgaga gtgcccatcg gctgaagtca agcatcgggc tgatcaatga 1050  
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aggacactcc cgagtttttt atagaccaag gccatgccaa ggtggcccaa 1150  
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caccctgggc atcgaagcca gctcggaagc tcagttttac accaaagggtg 1250  
accaacttat actcaacttg aataacatca gctctgatcg gatccagctg 1300  
atgaactctg ggattggctg gttccaacct gatgttctga aaaacatcat 1350  
cactgagatc atccactcca tcctgctgcc gaaccagaat ggcaaattaa 1400  
gatctggggg ccagtgctca ttggtgaagg ccttgggatt cgaggcagct 1450

gagtcctcac tgaccaagga tgcccttggtg cttactccag cctccttggtg 1500  
 gaaacccagc tctcctgtct ccagtggaag acttggtgag cagccatcag 1550  
 ggaaggctgg gtccagctg ggagtatggg tgtgagctct atagaccatc 1600  
 cctctctgca atcaataaac acttgctgtg gaaaaa 1636

<210> 128  
 <211> 484  
 <212> PRT  
 <213> Homo sapiens

<400> 128  
 Met Ala Gly Pro Trp Thr Phe Thr Leu Leu Cys Gly Leu Leu Ala  
 1 5 10 15  
 Ala Thr Leu Ile Gln Ala Thr Leu Ser Pro Thr Ala Val Leu Ile  
 20 25 30  
 Leu Gly Pro Lys Val Ile Lys Glu Lys Leu Thr Gln Glu Leu Lys  
 35 40 45  
 Asp His Asn Ala Thr Ser Ile Leu Gln Gln Leu Pro Leu Leu Ser  
 50 55 60  
 Ala Met Arg Glu Lys Pro Ala Gly Gly Ile Pro Val Leu Gly Ser  
 65 70 75  
 Leu Val Asn Thr Val Leu Lys His Ile Ile Trp Leu Lys Val Ile  
 80 85 90  
 Thr Ala Asn Ile Leu Gln Leu Gln Val Lys Pro Ser Ala Asn Asp  
 95 100 105  
 Gln Glu Leu Leu Val Lys Ile Pro Leu Asp Met Val Ala Gly Phe  
 110 115 120  
 Asn Thr Pro Leu Val Lys Thr Ile Val Glu Phe His Met Thr Thr  
 125 130 135  
 Glu Ala Gln Ala Thr Ile Arg Met Asp Thr Ser Ala Ser Gly Pro  
 140 145 150  
 Thr Arg Leu Val Leu Ser Asp Cys Ala Thr Ser His Gly Ser Leu  
 155 160 165  
 Arg Ile Gln Leu Leu Tyr Lys Leu Ser Phe Leu Val Asn Ala Leu  
 170 175 180  
 Ala Lys Gln Val Met Asn Leu Leu Val Pro Ser Leu Pro Asn Leu  
 185 190 195  
 Val Lys Asn Gln Leu Cys Pro Val Ile Glu Ala Ser Phe Asn Gly  
 200 205 210  
 Met Tyr Ala Asp Leu Leu Gln Leu Val Lys Val Pro Ile Ser Leu  
 215 220 225

Ser Ile Asp Arg Leu Glu Phe Asp Leu Leu Tyr Pro Ala Ile Lys  
230 235 240

Gly Asp Thr Ile Gln Leu Tyr Leu Gly Ala Lys Leu Leu Asp Ser  
245 250 255

Gln Gly Lys Val Thr Lys Trp Phe Asn Asn Ser Ala Ala Ser Leu  
260 265 270

Thr Met Pro Thr Leu Asp Asn Ile Pro Phe Ser Leu Ile Val Ser  
275 280 285

Gln Asp Val Val Lys Ala Ala Val Ala Ala Val Leu Ser Pro Glu  
290 295 300

Glu Phe Met Val Leu Leu Asp Ser Val Leu Pro Glu Ser Ala His  
305 310 315

Arg Leu Lys Ser Ser Ile Gly Leu Ile Asn Glu Lys Ala Ala Asp  
320 325 330

Lys Leu Gly Ser Thr Gln Ile Val Lys Ile Leu Thr Gln Asp Thr  
335 340 345

Pro Glu Phe Phe Ile Asp Gln Gly His Ala Lys Val Ala Gln Leu  
350 355 360

Ile Val Leu Glu Val Phe Pro Ser Ser Glu Ala Leu Arg Pro Leu  
365 370 375

Phe Thr Leu Gly Ile Glu Ala Ser Ser Glu Ala Gln Phe Tyr Thr  
380 385 390

Lys Gly Asp Gln Leu Ile Leu Asn Leu Asn Asn Ile Ser Ser Asp  
395 400 405

Arg Ile Gln Leu Met Asn Ser Gly Ile Gly Trp Phe Gln Pro Asp  
410 415 420

Val Leu Lys Asn Ile Ile Thr Glu Ile Ile His Ser Ile Leu Leu  
425 430 435

Pro Asn Gln Asn Gly Lys Leu Arg Ser Gly Val Pro Val Ser Leu  
440 445 450

Val Lys Ala Leu Gly Phe Glu Ala Ala Glu Ser Ser Leu Thr Lys  
455 460 465

Asp Ala Leu Val Leu Thr Pro Ala Ser Leu Trp Lys Pro Ser Ser  
470 475 480

Pro Val Ser Gln

- <210> 129
- <211> 2213
- <212> DNA
- <213> Homo sapiens

<400> 129

gagcgaacat ggcagcgcgt tggcggtttt ggtgtgtctc tgtgaccatg 50  
 gtggtggcgc tgctcatcgt ttgcgacgtt ccctcagcct ctgccccaaag 100  
 aaagaaggag atggtgttat ctgaaaaggt tagtcagctg atggaatgga 150  
 ctaacaaaag acctgtaata agaataaatg gagacaagtt ccgtcgcctt 200  
 gtgaaagccc caccgagaaa ttactccgtt atcgtcatgt tcaactgctct 250  
 ccaactgcat agacagtgtg tcgtttgcaa gcaagctgat gaagaattcc 300  
 agatcctggc aaactcctgg cgatactcca gtgcattcac caacaggata 350  
 ttttttgcca tgggtggattt tgatgaaggc tctgatgtat ttcagatgct 400  
 aaacatgaat tcagctccaa ctttcatcaa ctttcctgca aaagggaac 450  
 ccaaacgggg tgatacatat gagttacagg tgcggggttt ttcagctgag 500  
 cagattgccc ggtggatcgc cgacagaact gatgtcaata ttagagtgat 550  
 tagaccccc aattatgctg gtccccttat gttgggattg cttttggctg 600  
 ttattggtgg acttgtgtat cttcgaagaa gtaatatgga atttctcttt 650  
 aataaaaactg gatgggcttt tgcagctttg tgttttgtgc ttgctatgac 700  
 atctggtcaa atgtggaacc atataagagg accaccatat gcccataaga 750  
 atccccacac gggacatgtg aattatatcc atggaagcag tcaagcccag 800  
 tttgtagctg aaacacacat tgttcttctg tttaatggtg gagttacctt 850  
 aggaatggtg cttttatgtg aagctgctac ctctgacatg gatattggaa 900  
 agcgaaagat aatgtgtgtg gctggatttg gacttgttgt attattcttc 950  
 agttggatgc tctctatttt tagatctaaa tatcatggct acccatacag 1000  
 ctttctgatg agttaaaaag gtcccagaga tatatagaca ctggagtact 1050  
 ggaaattgaa aaacgaaaat cgtgtgtgtt tgaaaagaag aatgcaactt 1100  
 gtatatattt tattacctct ttttttcaag tgatttaaag agttaatcat 1150  
 ttaaccaaag aagatgtgta gtgccttaac aagcaatcct ctgtcaaaaat 1200  
 ctgaggtatt tgaaaataat tatcctctta accttctctt ccagtgaaac 1250  
 tttatggaac atttaattta gtacaattaa gtatattata aaaattgtaa 1300  
 aactactact ttgttttagt tagaaciaag ctcaaaaacta ctttagttaa 1350  
 cttggtcatc tgattttata ttgccttacc caaagatggg gaaagtaagt 1400  
 cctgaccagg tgttcccaca tatgcctgtt acagataact acattaggaa 1450







tcagaaccgc taccggcgat gctactgctg tgggtgtcgg tggtcgcagc 150  
 cttggcgctg gcggtactgg ccccgaggc aggggagcag aggcggagag 200  
 cagccaaagc gcccaatgtg gtgctggctg tgagcgactc cttcgatgga 250  
 aggttaacat ttcattccagg aagtcaggta gtgaaacttc cttttatcaa 300  
 ctttatgaag acacgtggga cttcctttct gaatgcctac acaaactctc 350  
 caatttggtg cccatcacgc gcagcaatgt ggagtggcct cttcactcac 400  
 ttaacagaat cttggaataa ttttaagggc ctagatccaa attatacaac 450  
 atggatggat gtcattggaga ggcattggcta ccgaacacag aaatttgga 500  
 aactggacta tacttcagga catcactcca ttagtaatcg tgtggaagcg 550  
 tggacaagag atgttgcttt cttactcaga caagaaggca ggcccatggt 600  
 taatcttatt cgtaacagga ctaaagtcag agtgatggaa agggattggc 650  
 agaatacaga caaagcagta aactgggttaa gaaaggaagc aattaattac 700  
 actgaaccat ttgttattta cttgggatta aatttaccac acccttacc 750  
 ttcaccatct tctggagaaa attttggtatc ttcaacattt cacacatctc 800  
 tttattggct tgaaaaagtg tctcatgatg ccatcaaat cccaaagtgg 850  
 tcacctttgt cagaaatgca cctgtagat tattactctt cttatacaaa 900  
 aaactgcact ggaagattta caaaaaaaga aattaagaat attagagcat 950  
 tttattatgc tatgtgtgct gagacagatg ccatgcttgg tgaaattatt 1000  
 ttggcccttc atcaattaga tcttcttcag aaaactattg tcatatactc 1050  
 ctcagaccat ggagagctgg ccatggaaca tgcagagttt tataaaatga 1100  
 gcatgtacga ggctagtgc catgttccgc ttttgatgat gggaccagga 1150  
 attaaagccg gcctacaagt atcaaagtgt gtttctcttg tggatattta 1200  
 ccctaccatg cttgatattg ctggaattcc tctgcctcag aacctgagt 1250  
 gatactcttt gttgccgtta tcatcagaaa catttaagaa tgaacataaa 1300  
 gtcaaaaacc tgcatccacc ctggattctg agtgaattcc atggatgtaa 1350  
 tgtgaatgcc tccacctaca tgcttcgaac taaccactgg aaatatatag 1400  
 cctattcgga tggatcatca atattgcctc aactctttga tctttcctcg 1450  
 gatccagatg aattaacaaa tgttgctgta aaatttccag aaattactta 1500  
 ttccttggat cagaagcttc attccattat aaactaccct aaagtttctg 1550



Asn	Ser	Pro	Ile	Cys	Cys	Pro	Ser	Arg	Ala	Ala	Met	Trp	Ser	Gly	
				80					85					90	
Leu	Phe	Thr	His	Leu	Thr	Glu	Ser	Trp	Asn	Asn	Phe	Lys	Gly	Leu	
				95					100					105	
Asp	Pro	Asn	Tyr	Thr	Thr	Trp	Met	Asp	Val	Met	Glu	Arg	His	Gly	
				110					115					120	
Tyr	Arg	Thr	Gln	Lys	Phe	Gly	Lys	Leu	Asp	Tyr	Thr	Ser	Gly	His	
				125					130					135	
His	Ser	Ile	Ser	Asn	Arg	Val	Glu	Ala	Trp	Thr	Arg	Asp	Val	Ala	
				140					145					150	
Phe	Leu	Leu	Arg	Gln	Glu	Gly	Arg	Pro	Met	Val	Asn	Leu	Ile	Arg	
				155					160					165	
Asn	Arg	Thr	Lys	Val	Arg	Val	Met	Glu	Arg	Asp	Trp	Gln	Asn	Thr	
				170					175					180	
Asp	Lys	Ala	Val	Asn	Trp	Leu	Arg	Lys	Glu	Ala	Ile	Asn	Tyr	Thr	
				185					190					195	
Glu	Pro	Phe	Val	Ile	Tyr	Leu	Gly	Leu	Asn	Leu	Pro	His	Pro	Tyr	
				200					205					210	
Pro	Ser	Pro	Ser	Ser	Gly	Glu	Asn	Phe	Gly	Ser	Ser	Thr	Phe	His	
				215					220					225	
Thr	Ser	Leu	Tyr	Trp	Leu	Glu	Lys	Val	Ser	His	Asp	Ala	Ile	Lys	
				230					235					240	
Ile	Pro	Lys	Trp	Ser	Pro	Leu	Ser	Glu	Met	His	Pro	Val	Asp	Tyr	
				245					250					255	
Tyr	Ser	Ser	Tyr	Thr	Lys	Asn	Cys	Thr	Gly	Arg	Phe	Thr	Lys	Lys	
				260					265					270	
Glu	Ile	Lys	Asn	Ile	Arg	Ala	Phe	Tyr	Tyr	Ala	Met	Cys	Ala	Glu	
				275					280					285	
Thr	Asp	Ala	Met	Leu	Gly	Glu	Ile	Ile	Leu	Ala	Leu	His	Gln	Leu	
				290					295					300	
Asp	Leu	Leu	Gln	Lys	Thr	Ile	Val	Ile	Tyr	Ser	Ser	Asp	His	Gly	
				305					310					315	
Glu	Leu	Ala	Met	Glu	His	Arg	Gln	Phe	Tyr	Lys	Met	Ser	Met	Tyr	
				320					325					330	
Glu	Ala	Ser	Ala	His	Val	Pro	Leu	Leu	Met	Met	Gly	Pro	Gly	Ile	
				335					340					345	
Lys	Ala	Gly	Leu	Gln	Val	Ser	Asn	Val	Val	Ser	Leu	Val	Asp	Ile	
				350					355					360	
Tyr	Pro	Thr	Met	Leu	Asp	Ile	Ala	Gly	Ile	Pro	Leu	Pro	Gln	Asn	





	50	55	60
Ile Thr Gln Cys Asp	Ile Tyr Ser Thr	Leu Leu Gly Leu Pro	Ala
65	70	75	
Asp Ile Gln Ala Ala	Gln Ala Met Met	Val Thr Ser Ser Ala	Ile
80	85	90	
Ser Ser Leu Ala Cys	Ile Ile Ser Val	Val Gly Met Arg Cys	Thr
95	100	105	
Val Phe Cys Gln Glu	Ser Arg Ala Lys	Asp Arg Val Ala Val	Ala
110	115	120	
Gly Gly Val Phe Phe	Ile Leu Gly Gly	Leu Leu Gly Phe Ile	Pro
125	130	135	
Val Ala Trp Asn Leu	His Gly Ile Leu	Arg Asp Phe Tyr Ser	Pro
140	145	150	
Leu Val Pro Asp Ser	Met Lys Phe Glu	Ile Gly Glu Ala Leu	Tyr
155	160	165	
Leu Gly Ile Ile Ser	Ser Leu Phe Ser	Leu Ile Ala Gly Ile	Ile
170	175	180	
Leu Cys Phe Ser Cys	Ser Ser Gln Arg	Asn Arg Ser Asn Tyr	Tyr
185	190	195	
Asp Ala Tyr Gln Ala	Gln Pro Leu Ala	Thr Arg Ser Ser Pro	Arg
200	205	210	
Pro Gly Gln Pro Pro	Lys Val Lys Ser	Glu Phe Asn Ser Tyr	Ser
215	220	225	
Leu Thr Gly Tyr Val			
230			

<210> 135  
 <211> 610  
 <212> DNA  
 <213> Homo sapiens

<400> 135  
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 aagtcacgc tcccgtggc tcagaacct ggctgtgcca gccggcacc 150  
 aggtgtggag acaagatcta caacccttg gagcagtgct gttacaatga 200  
 cgccatcgtg tccctgagcg agaccgcca atgtggtccc ccctgcacct 250  
 tctggccctg ctttgagctc tgctgtcttg attcctttgg cctcaciaaac 300  
 gattttgttg tgaagctgaa gggtcagggt gtgaattccc agtgccactc 350

atctcccatc tccagtaa at gtgaaagcag aagacgtttt ccctgagaag 400  
 acatagaaag aaaatcaact ttcactaagg catctcagaa acataggcta 450  
 aggtaatatg tgtaccagta gagaagcctg aggaattttac aaaatgatgc 500  
 agctccaagc cattgtatgg cccatgtggg agactgatgg gacatggaga 550  
 atgacagtag attatcagga aataaataaa gtgggttttc caatgtacac 600  
 acctgtaaaa 610

<210> 136  
 <211> 119  
 <212> PRT  
 <213> Homo sapiens

<400> 136  
 Met Val Pro Arg Ile Phe Ala Pro Ala Tyr Val Ser Val Cys Leu  
   1                  5                  10                  15  
 Leu Leu Leu Cys Pro Arg Glu Val Ile Ala Pro Ala Gly Ser Glu  
                   20                  25                  30  
 Pro Trp Leu Cys Gln Pro Ala Pro Arg Cys Gly Asp Lys Ile Tyr  
                   35                  40                  45  
 Asn Pro Leu Glu Gln Cys Cys Tyr Asn Asp Ala Ile Val Ser Leu  
                   50                  55                  60  
 Ser Glu Thr Arg Gln Cys Gly Pro Pro Cys Thr Phe Trp Pro Cys  
                   65                  70                  75  
 Phe Glu Leu Cys Cys Leu Asp Ser Phe Gly Leu Thr Asn Asp Phe  
                   80                  85                  90  
 Val Val Lys Leu Lys Val Gln Gly Val Asn Ser Gln Cys His Ser  
                   95                  100                  105  
 Ser Pro Ile Ser Ser Lys Cys Glu Ser Arg Arg Arg Phe Pro  
                   110                  115

<210> 137  
 <211> 771  
 <212> DNA  
 <213> Homo sapiens

<400> 137  
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 gtcttttgcca ttttctgcat ctccaggctc ctctgctcac acggagcccc 100  
 agtggccccc atgactcctt acctgatgct gtgccagcca cacaagagat 150  
 gtggggacaa gttctacgac cccctgcagc actgttgcta tgatgatgcc 200  
 gtcgtgccct tggccaggac ccagacgtgt ggaaactgca ccttcagagt 250

ctgctttgag cagtgtgcc cctggacctt catggtgaag ctgataaacc 300  
 agaactgcga ctcagcccg acctcggatg acaggctttg tcgcagtgtc 350  
 agctaattgga acatcagggg aacgatgact cctggattct ctttcctggg 400  
 tgggcctgga gaaagaggct ggtgttacct gagatctggg atgctgagt 450  
 gctgtttggg ggccagagaa acacacactc aactgcccac ttcattctgt 500  
 gacctgtctg aggcccaccc tgcagctgcc ctgaggaggc ccacaggtcc 550  
 ctttctagaa ttctggacag catgagatgc gtgtgctgat gggggcccag 600  
 ggactctgaa ccctcctgat gaccctatg gccaacatca acccggcacc 650  
 accccaaggc tggctgggga acccttcacc cttctgtgag attttccatc 700  
 atctcaagtt ctcttctatc caggagcaaa gcacaggatc ataataaatt 750  
 tatgtacttt ataaatgaaa a 771

<210> 138  
 <211> 110  
 <212> PRT  
 <213> Homo sapiens

<400> 138  
 Met Ala Pro Arg Gly Cys Ile Val Ala Val Phe Ala Ile Phe Cys  
     1                    5                    10                    15  
 Ile Ser Arg Leu Leu Cys Ser His Gly Ala Pro Val Ala Pro Met  
                     20                    25                    30  
 Thr Pro Tyr Leu Met Leu Cys Gln Pro His Lys Arg Cys Gly Asp  
                     35                    40                    45  
 Lys Phe Tyr Asp Pro Leu Gln His Cys Cys Tyr Asp Asp Ala Val  
                     50                    55                    60  
 Val Pro Leu Ala Arg Thr Gln Thr Cys Gly Asn Cys Thr Phe Arg  
                     65                    70                    75  
 Val Cys Phe Glu Gln Cys Cys Pro Trp Thr Phe Met Val Lys Leu  
                     80                    85                    90  
 Ile Asn Gln Asn Cys Asp Ser Ala Arg Thr Ser Asp Asp Arg Leu  
                     95                    100                    105  
 Cys Arg Ser Val Ser  
                     110

<210> 139  
 <211> 2044  
 <212> DNA  
 <213> Homo sapiens

<400> 139



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 ctccccggca ccagaagttc ctctgcgcgt ccgacggcga catgggcgtc 150  
 cccacggccc tggaggccgg cagctggcgc tggggatccc tgcctcttcgc 200  
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 gtcggcctcc gaccaccatg gcaacttctc catcaccatg cgcaacctga 550  
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 caccactcgg agcacagggt ccatgggtgc atggagctgc aggtgcagac 650  
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 ggaatcctct gcctccccct catcctgctc ctggtctaca agcaaaggca 800  
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 ttgtggctgg gtctggggca ggtgcatttg agccagggt ggctctgtga 1150  
 gtggcctcct tggcctcggc cctggttccc tccctcctgc tctgggctca 1200  
 gatactgtga catcccagaa gccagcccc tcaaccctc tggatgctac 1250  
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 agattctccc ctagagacct gaaattcacc agctacagat gccaaatgac 1350  
 ttacatctta agaagtctca gaacgtccag cccttcagca gctctcgttc 1400  
 tgagacatga gccttgggat gtggcagcat cagtgggaca agatggacac 1450

tggggccaccc tcccaggcac cagacacagg gcacggtgga gagacttctc 1500  
 ccccggtggcc gccttggctc ccccgttttg cccgaggctg ctctttctgtc 1550  
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 gggaaggtga gtggagaggg gcacctgccc cccgccctcc ccatccccta 1900  
 ctcccactgc tcagcgcggg ccattgcaag ggtgccacac aatgtcttgt 1950  
 ccaccctggg acacttctga gtatgaagcg ggatgctatt aaaaactaca 2000  
 tggggaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaga 2044

<210> 140

<211> 311

<212> PRT

<213> Homo sapiens

<400> 140

Met	Gly	Val	Pro	Thr	Ala	Leu	Glu	Ala	Gly	Ser	Trp	Arg	Trp	Gly
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Ser	Leu	Leu	Phe	Ala	Leu	Phe	Leu	Ala	Ala	Ser	Leu	Gly	Pro	Val
			20						25					30
Ala	Ala	Phe	Lys	Val	Ala	Thr	Pro	Tyr	Ser	Leu	Tyr	Val	Cys	Pro
			35						40					45
Glu	Gly	Gln	Asn	Val	Thr	Leu	Thr	Cys	Arg	Leu	Leu	Gly	Pro	Val
			50						55					60
Asp	Lys	Gly	His	Asp	Val	Thr	Phe	Tyr	Lys	Thr	Trp	Tyr	Arg	Ser
			65						70					75
Ser	Arg	Gly	Glu	Val	Gln	Thr	Cys	Ser	Glu	Arg	Arg	Pro	Ile	Arg
			80						85					90
Asn	Leu	Thr	Phe	Gln	Asp	Leu	His	Leu	His	His	Gly	Gly	His	Gln
			95						100					105
Ala	Ala	Asn	Thr	Ser	His	Asp	Leu	Ala	Gln	Arg	His	Gly	Leu	Glu
			110						115					120
Ser	Ala	Ser	Asp	His	His	Gly	Asn	Phe	Ser	Ile	Thr	Met	Arg	Asn
			125						130					135
Leu	Thr	Leu	Leu	Asp	Ser	Gly	Leu	Tyr	Cys	Cys	Leu	Val	Val	Glu

140	145	150
Ile Arg His His His Ser Glu His Arg Val His Gly Ala Met Glu		
155	160	165
Leu Gln Val Gln Thr Gly Lys Asp Ala Pro Ser Asn Cys Val Val		
170	175	180
Tyr Pro Ser Ser Ser Gln Asp Ser Glu Asn Ile Thr Ala Ala Ala		
185	190	195
Leu Ala Thr Gly Ala Cys Ile Val Gly Ile Leu Cys Leu Pro Leu		
200	205	210
Ile Leu Leu Leu Val Tyr Lys Gln Arg Gln Ala Ala Ser Asn Arg		
215	220	225
Arg Ala Gln Glu Leu Val Arg Met Asp Ser Asn Ile Gln Gly Ile		
230	235	240
Glu Asn Pro Gly Phe Glu Ala Ser Pro Pro Ala Gln Gly Ile Pro		
245	250	255
Glu Ala Lys Val Arg His Pro Leu Ser Tyr Val Ala Gln Arg Gln		
260	265	270
Pro Ser Glu Ser Gly Arg His Leu Leu Ser Glu Pro Ser Thr Pro		
275	280	285
Leu Ser Pro Pro Gly Pro Gly Asp Val Phe Phe Pro Ser Leu Asp		
290	295	300
Pro Val Pro Asp Ser Pro Asn Phe Glu Val Ile		
305	310	

<210> 141  
 <211> 1732  
 <212> DNA  
 <213> Homo sapiens

<400> 141  
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 cttagacctc ccttctgccc ctcttttctt gccaccgct gcttctggc 150  
 ccttctccga cccgcgtcta gcagcagacc tcttgggggc tgtgggttga 200  
 tctgtggccc ctgtgcctcc gtgtcctttt cgtctccctt cctcccgaact 250  
 ccgctcccgg accagcggcc tgaccctggg gaaaggatgg ttcccgaagt 300  
 gagggctctc tctctcttgc tgggactcgc gctgctctgg ttccccctgg 350  
 actcccacgc tcgagcccgc ccagacatgt tctgcctttt ccatgggaag 400  
 agatactccc cggcgagag ctggcaccct tacttgagc cacaaggcct 450

gatgtactgc ctgcgctgta cctgctcaga gggcgcccat gtgagttgtt 500  
 accgcctcca ctgtccgcct gtccactgcc cccagcctgt gacggagcca 550  
 cagcaatgct gtcccaagtg tgtggaacct cacactccct ctggactccg 600  
 ggccccacca aagtccctgcc agcacaacgg gaccatgtac caacacggag 650  
 agatcttcag tgcccatgag ctgttcccct cccgcctgcc caaccagtgt 700  
 gtcctctgca gctgcacaga gggccagatc tactgcggcc tcacaacctg 750  
 ccccgaaacca ggctgccag caccctccc actgccagac tcctgctgcc 800  
 aagcctgcaa agatgaggca agtgagcaat cggatgaaga ggacagtgtg 850  
 cagtcgctcc atggggtgag acatcctcag gatccatgtt ccagtgtatgc 900  
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 ctctgagctt catccctcgc cacttcagac ccaagggagc aggagcaca 1000  
 actgtcaaga tcgtcctgaa ggagaaacat aagaaagcct gtgtgcatgg 1050  
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 tcggccccctt gccctgcac ctatgcacct gtgaggatgg ccgccaggac 1150  
 tgccagcgtg tgacctgtcc caccgagtac cctgccgtc accccgagaa 1200  
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 gccacagtga gatcagttct accaggtgtc ccaaggcacc gggccgggtc 1300  
 ctcgccaca catcggtatc cccaagccca gacaacctgc gtcgctttgc 1350  
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 taaaagatga ggaaactgag gctcagagag gtgaagtacc tggcccaagg 1450  
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 aagacttcca gaaagaggca cagcacttcc gactgctcgc tggccccac 1550  
 gaaggctact ggaacgtctt cctagcccag accctggagc tgaaggtcac 1600  
 ggccagtcca gacaaagtga ccaagacata acaaagacct aacagttgca 1650  
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 cattaccctc aaaaaaaaaa aaaaaaaaaa aa 1732

<210> 142  
 <211> 451  
 <212> PRT  
 <213> Homo sapiens  
 <400> 142

Met	Val	Pro	Glu	Val	Arg	Val	Leu	Ser	Ser	Leu	Leu	Gly	Leu	Ala	
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Leu	Leu	Trp	Phe	Pro	Leu	Asp	Ser	His	Ala	Arg	Ala	Arg	Pro	Asp	
				20					25					30	
Met	Phe	Cys	Leu	Phe	His	Gly	Lys	Arg	Tyr	Ser	Pro	Gly	Glu	Ser	
				35					40					45	
Trp	His	Pro	Tyr	Leu	Glu	Pro	Gln	Gly	Leu	Met	Tyr	Cys	Leu	Arg	
				50					55					60	
Cys	Thr	Cys	Ser	Glu	Gly	Ala	His	Val	Ser	Cys	Tyr	Arg	Leu	His	
				65					70					75	
Cys	Pro	Pro	Val	His	Cys	Pro	Gln	Pro	Val	Thr	Glu	Pro	Gln	Gln	
				80					85					90	
Cys	Cys	Pro	Lys	Cys	Val	Glu	Pro	His	Thr	Pro	Ser	Gly	Leu	Arg	
				95					100					105	
Ala	Pro	Pro	Lys	Ser	Cys	Gln	His	Asn	Gly	Thr	Met	Tyr	Gln	His	
				110					115					120	
Gly	Glu	Ile	Phe	Ser	Ala	His	Glu	Leu	Phe	Pro	Ser	Arg	Leu	Pro	
				125					130					135	
Asn	Gln	Cys	Val	Leu	Cys	Ser	Cys	Thr	Glu	Gly	Gln	Ile	Tyr	Cys	
				140					145					150	
Gly	Leu	Thr	Thr	Cys	Pro	Glu	Pro	Gly	Cys	Pro	Ala	Pro	Leu	Pro	
				155					160					165	
Leu	Pro	Asp	Ser	Cys	Cys	Gln	Ala	Cys	Lys	Asp	Glu	Ala	Ser	Glu	
				170					175					180	
Gln	Ser	Asp	Glu	Glu	Asp	Ser	Val	Gln	Ser	Leu	His	Gly	Val	Arg	
				185					190					195	
His	Pro	Gln	Asp	Pro	Cys	Ser	Ser	Asp	Ala	Gly	Arg	Lys	Arg	Gly	
				200					205					210	
Pro	Gly	Thr	Pro	Ala	Pro	Thr	Gly	Leu	Ser	Ala	Pro	Leu	Ser	Phe	
				215					220					225	
Ile	Pro	Arg	His	Phe	Arg	Pro	Lys	Gly	Ala	Gly	Ser	Thr	Thr	Val	
				230					235					240	
Lys	Ile	Val	Leu	Lys	Glu	Lys	His	Lys	Lys	Ala	Cys	Val	His	Gly	
				245					250					255	
Gly	Lys	Thr	Tyr	Ser	His	Gly	Glu	Val	Trp	His	Pro	Ala	Phe	Arg	
				260					265					270	
Ala	Phe	Gly	Pro	Leu	Pro	Cys	Ile	Leu	Cys	Thr	Cys	Glu	Asp	Gly	
				275					280					285	
Arg	Gln	Asp	Cys	Gln	Arg	Val	Thr	Cys	Pro	Thr	Glu	Tyr	Pro	Cys	

290	295	300
Arg His Pro Glu Lys Val Ala Gly Lys Cys Cys Lys Ile Cys Pro		
305	310	315
Glu Asp Lys Ala Asp Pro Gly His Ser Glu Ile Ser Ser Thr Arg		
320	325	330
Cys Pro Lys Ala Pro Gly Arg Val Leu Val His Thr Ser Val Ser		
335	340	345
Pro Ser Pro Asp Asn Leu Arg Arg Phe Ala Leu Glu His Glu Ala		
350	355	360
Ser Asp Leu Val Glu Ile Tyr Leu Trp Lys Leu Val Lys Asp Glu		
365	370	375
Glu Thr Glu Ala Gln Arg Gly Glu Val Pro Gly Pro Arg Pro His		
380	385	390
Ser Gln Asn Leu Pro Leu Asp Ser Asp Gln Glu Ser Gln Glu Ala		
395	400	405
Arg Leu Pro Glu Arg Gly Thr Ala Leu Pro Thr Ala Arg Trp Pro		
410	415	420
Pro Arg Arg Ser Leu Glu Arg Leu Pro Ser Pro Asp Pro Gly Ala		
425	430	435
Glu Gly His Gly Gln Ser Arg Gln Ser Asp Gln Asp Ile Thr Lys		
440	445	450

Thr

<210> 143  
 <211> 693  
 <212> DNA  
 <213> Homo sapiens

<400> 143  
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 cttgcggaaa atgctgatct cagtcgcaat gctgggcgca ggggctggcg 150  
 tgggctacgc gctcctcggt atcgtgacct cgaggagagc gcggaagcag 200  
 gaaatgctaa aggagatgcc actgcaggac ccaaggagca gggaggaggc 250  
 ggccaggacc cagcagctat tgctggccac tctgcaggag gcagcgacca 300  
 cgcaggagaa cgtggcctgg aggaagaact ggatggttgg cggcgaaggc 350  
 ggcgccagcg ggaggtcacc gtgagaccgg acttgccctc gtgggcgccg 400  
 gaccttggct tgggcgcagg aatccgaggc agcctttctc cttcgtgggc 450

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 gtgagctgcc gtcgggtgag cacgtttccc ccaaaccctg gactgactgc 550  
 ttttaagggtcc gcaaggcggg ccagggccga gacgcgagtc ggatgtggtg 600  
 aactgaaaga accaataaaa tcatgttcct ccaaaaaaaaaa aaaaaaaaaa 650  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 693

<210> 144  
 <211> 93  
 <212> PRT  
 <213> Homo sapiens

<400> 144  
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 20 25 30  
 Gly Glu Arg Arg Lys Gln Glu Met Leu Lys Glu Met Pro Leu Gln  
 35 40 45  
 Asp Pro Arg Ser Arg Glu Glu Ala Ala Arg Thr Gln Gln Leu Leu  
 50 55 60  
 Leu Ala Thr Leu Gln Glu Ala Ala Thr Thr Gln Glu Asn Val Ala  
 65 70 75  
 Trp Arg Lys Asn Trp Met Val Gly Gly Glu Gly Gly Ala Ser Gly  
 80 85 90  
 Arg Ser Pro

<210> 145  
 <211> 1883  
 <212> DNA  
 <213> Homo sapiens

<400> 145  
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 caggctgcca tggggcccag caccctctc ctcactctgt tccttttgtc 150  
 atggtcggga cccctccaag gacagcagca ccaccttgtg gactacatgg 200  
 aacgcgcgact agctgcttta gaggaacggc tggcccagtg ccaggaccag 250  
 agtagtcggc atgctgctga gctgcgggac ttcaagaaca agatgctgcc 300  
 actgctggag gtggcagaga aggagcggga ggcactcaga actgaggccg 350  
 acaccatctc cgggagagtg gatcgtctgg agcgggaggt agactatctg 400

gagaccaga accagctct gccctgtgta gagtttgatg agaaggtgac 450  
 tggaggccct gggaccaaag gcaagggag aaggaatgag aagtacgata 500  
 tggtgacaga ctgtggctac acaatctctc aagtgagatc aatgaagatt 550  
 ctgaagcgat ttggtggccc agctggtcta tggaccaagg atccactggg 600  
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 ttgtcttccc aaggctgcgt gacttcaccc ttgccatggc tgcccggaaa 700  
 gcttcccagag tccgggtgcc cttcccctgg gtaggcacag ggcagctggt 750  
 atatggtggc tttctttatt ttgctcggag gcctcctgga agacctggtg 800  
 gaggtggtga gatggagaac actttgcagc taatcaaatt ccacctggca 850  
 aaccgaacag tgggtggacag ctcagtattc ccagcagagg ggctgatccc 900  
 cccctacggc ttgacagcag acacctacat cgacctggta gctgatgagg 950  
 aaggctcttg ggctgtctat gccaccggg aggatgacag gcacttgtgt 1000  
 ctggccaagt tagatccaca gacactggac acagagcagc agtgggacac 1050  
 accatgtccc agagagaatg ctgaggctgc ctttgtcatc tgtgggaccc 1100  
 tctatgtcgt ctataacacc cgtcctgcca gtcggggccg catccagtgc 1150  
 tcctttgatg ccagcggcac cctgacctt gaacgggcag cactccctta 1200  
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 gagatgagga agaaagagga ggaggtttga ggagctagcc ttgttttttg 1350  
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 ttcttcattc ttcaaatgtg ggccagttgt ggctcaaate ctctatattt 1450  
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 cccagacca gggctctaac cttgtatggc ggcaggccca gggagcaggc 1650  
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 acgtccagct ctgtcctctc ttctcaact cctccttcag tgtcctgagg 1750  
 aacaggactt tctccacatt gttttgtatt gcaacatttt gcattaaaag 1800  
 gaaaatccac aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1850



aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaa 1883

<210> 146

<211> 406

<212> PRT

<213> Homo sapiens

<400> 146

Met	Gly	Pro	Ser	Thr	Pro	Leu	Leu	Ile	Leu	Phe	Leu	Leu	Ser	Trp
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Ser	Gly	Pro	Leu	Gln	Gly	Gln	Gln	His	His	Leu	Val	Glu	Tyr	Met
				20					25					30
Glu	Arg	Arg	Leu	Ala	Ala	Leu	Glu	Glu	Arg	Leu	Ala	Gln	Cys	Gln
				35					40					45
Asp	Gln	Ser	Ser	Arg	His	Ala	Ala	Glu	Leu	Arg	Asp	Phe	Lys	Asn
				50					55					60
Lys	Met	Leu	Pro	Leu	Leu	Glu	Val	Ala	Glu	Lys	Glu	Arg	Glu	Ala
				65					70					75
Leu	Arg	Thr	Glu	Ala	Asp	Thr	Ile	Ser	Gly	Arg	Val	Asp	Arg	Leu
				80					85					90
Glu	Arg	Glu	Val	Asp	Tyr	Leu	Glu	Thr	Gln	Asn	Pro	Ala	Leu	Pro
				95					100					105
Cys	Val	Glu	Phe	Asp	Glu	Lys	Val	Thr	Gly	Gly	Pro	Gly	Thr	Lys
				110					115					120
Gly	Lys	Gly	Arg	Arg	Asn	Glu	Lys	Tyr	Asp	Met	Val	Thr	Asp	Cys
				125					130					135
Gly	Tyr	Thr	Ile	Ser	Gln	Val	Arg	Ser	Met	Lys	Ile	Leu	Lys	Arg
				140					145					150
Phe	Gly	Gly	Pro	Ala	Gly	Leu	Trp	Thr	Lys	Asp	Pro	Leu	Gly	Gln
				155					160					165
Thr	Glu	Lys	Ile	Tyr	Val	Leu	Asp	Gly	Thr	Gln	Asn	Asp	Thr	Ala
				170					175					180
Phe	Val	Phe	Pro	Arg	Leu	Arg	Asp	Phe	Thr	Leu	Ala	Met	Ala	Ala
				185					190					195
Arg	Lys	Ala	Ser	Arg	Val	Arg	Val	Pro	Phe	Pro	Trp	Val	Gly	Thr
				200					205					210
Gly	Gln	Leu	Val	Tyr	Gly	Gly	Phe	Leu	Tyr	Phe	Ala	Arg	Arg	Pro
				215					220					225
Pro	Gly	Arg	Pro	Gly	Gly	Gly	Gly	Glu	Met	Glu	Asn	Thr	Leu	Gln
				230					235					240
Leu	Ile	Lys	Phe	His	Leu	Ala	Asn	Arg	Thr	Val	Val	Asp	Ser	Ser
				245					250					255

Val	Phe	Pro	Ala	Glu	Gly	Leu	Ile	Pro	Pro	Tyr	Gly	Leu	Thr	Ala	
				260					265					270	
Asp	Thr	Tyr	Ile	Asp	Leu	Val	Ala	Asp	Glu	Glu	Gly	Leu	Trp	Ala	
				275					280					285	
Val	Tyr	Ala	Thr	Arg	Glu	Asp	Asp	Arg	His	Leu	Cys	Leu	Ala	Lys	
				290					295					300	
Leu	Asp	Pro	Gln	Thr	Leu	Asp	Thr	Glu	Gln	Gln	Trp	Asp	Thr	Pro	
				305					310					315	
Cys	Pro	Arg	Glu	Asn	Ala	Glu	Ala	Ala	Phe	Val	Ile	Cys	Gly	Thr	
				320					325					330	
Leu	Tyr	Val	Val	Tyr	Asn	Thr	Arg	Pro	Ala	Ser	Arg	Ala	Arg	Ile	
				335					340					345	
Gln	Cys	Ser	Phe	Asp	Ala	Ser	Gly	Thr	Leu	Thr	Pro	Glu	Arg	Ala	
				350					355					360	
Ala	Leu	Pro	Tyr	Phe	Pro	Arg	Arg	Tyr	Gly	Ala	His	Ala	Ser	Leu	
				365					370					375	
Arg	Tyr	Asn	Pro	Arg	Glu	Arg	Gln	Leu	Tyr	Ala	Trp	Asp	Asp	Gly	
				380					385					390	
Tyr	Gln	Ile	Val	Tyr	Lys	Leu	Glu	Met	Arg	Lys	Lys	Glu	Glu	Glu	
				395					400					405	

Val

<210> 147  
 <211> 2052  
 <212> DNA  
 <213> Homo sapiens

<400> 147  
 gacagctgtg tctcgatgga gtagactctc agaacagcgc agtttgcctt 50  
 ccgctcagcg agagcctctc cgtggcttcc gcaccttgag cattaggcca 100  
 gttctcctct tctctctaatt ccatccgtca cctctcctgt catccgtttc 150  
 catgccgtga ggtccattca cagaacacat ccatggctct catgctcagt 200  
 ttggttctga gtctcctcaa gctgggatca gggcagtggc aggtgtttgg 250  
 gccagacaag cctgtccagg ccttggtggg ggaggacgca gcattctcct 300  
 gtttcctgtc tcctaagacc aatgcagagg ccatggaagt gcggttcttc 350  
 aggggccagt tctctagcgt ggtccacctc tacagggacg ggaaggacca 400  
 gccatttatg cagatgccac agtatcaagg caggacaaaa ctggtgaagg 450  
 attctattgc ggagggggcg atctctctga ggctggaaaa cattactgtg 500

ttggatgctg gcctctatgg gtgcaggatt agttcccagt cttactacca 550  
 gaaggccatc tgggagctac aggtgtcagc actgggctca gttcctctca 600  
 tttccatcac gggatatgtt gatagagaca tccagctact ctgtcagtcc 650  
 tcgggctggt tccccgggc cacagcgaag tggaaaggct cacaaggaca 700  
 ggatttgtcc acagactcca ggacaaacag agacatgcat ggctgtttg 750  
 atgtggagat ctctctgacc gtccaagaga acgccgggag catatcctgt 800  
 tccatgcggc atgctcatct gagccgagag gtggaatcca gggtagagat 850  
 aggagatacc tttttcgagc ctatatcgtg gcacctggct accaaagtac 900  
 tgggaatact ctgctgtggc ctatTTTTTg gcattgttgg actgaagatt 950  
 ttcttctcca aattccagtg gaaaatccag gcggaactgg actggagaag 1000  
 aaagcacgga caggcagaat tgagagacgc ccggaacac gcagtggagg 1050  
 tgactctgga tccagagacg gctcaccga agctctgctt ttctgatctg 1100  
 aaaactgtaa cccatagaaa agctccccag gaggtgcctc actctgagaa 1150  
 gagatttaca aggaagagtg tgggtggcttc tcagagtttc caagcagggg 1200  
 aacattactg ggaggtggac ggaggacaca ataaaagggt gcgctgggga 1250  
 gtgtgccggg atgatgtgga caggaggaag gaggtagtga ctttgtctcc 1300  
 cgatcatggg tactgggtcc tcagactgaa tggagaacat ttgtatttca 1350  
 cattaaatcc ccgttttata agcgtcttcc ccaggacccc acctacaaaa 1400  
 ataggggtct tcctggacta tgagtgtggg accatctcct tcttcaacat 1450  
 aaatgaccag tcccttattt ataccctgac atgtcgggtt gaaggcttat 1500  
 tgaggcccta cattgagtat ccgtcctata atgagcaaaa tggaactccc 1550  
 atagtcatct gccagtcac ccaggaatca gagaaagagg cctcttggca 1600  
 aagggcctct gcaatcccag agacaagcaa cagtgagtcc tcctcacagg 1650  
 caaccacgcc ctctctcccc aggggtgaaa tgtaggatga atcacatccc 1700  
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 atgggagtca ggtgtcatgg ctgccctgag ctgggaggga agaaggctga 1850  
 cattacattt agtttgctct cactccatct ggctaagtga tcttgaaata 1900  
 ccacctctca ggtgaagaac cgtcaggaat tcccatctca caggctgtgg 1950

tgtagattaa gtagacaagg aatgtgaata atgcttagat cttattgatg 2000  
acagagtgta tcctaattggt ttgttcatta tattacactt tcagtaaaaa 2050  
aa 2052

<210> 148  
<211> 500  
<212> PRT  
<213> Homo sapiens

<400> 148

Met	Ala	Leu	Met	Leu	Ser	Leu	Val	Leu	Ser	Leu	Leu	Lys	Leu	Gly	1	5	10	15
Ser	Gly	Gln	Trp	Gln	Val	Phe	Gly	Pro	Asp	Lys	Pro	Val	Gln	Ala	20	25	30	
Leu	Val	Gly	Glu	Asp	Ala	Ala	Phe	Ser	Cys	Phe	Leu	Ser	Pro	Lys	35	40	45	
Thr	Asn	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Gly	Gln	Phe	50	55	60	
Ser	Ser	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Lys	Asp	Gln	Pro	Phe	65	70	75	
Met	Gln	Met	Pro	Gln	Tyr	Gln	Gly	Arg	Thr	Lys	Leu	Val	Lys	Asp	80	85	90	
Ser	Ile	Ala	Glu	Gly	Arg	Ile	Ser	Leu	Arg	Leu	Glu	Asn	Ile	Thr	95	100	105	
Val	Leu	Asp	Ala	Gly	Leu	Tyr	Gly	Cys	Arg	Ile	Ser	Ser	Gln	Ser	110	115	120	
Tyr	Tyr	Gln	Lys	Ala	Ile	Trp	Glu	Leu	Gln	Val	Ser	Ala	Leu	Gly	125	130	135	
Ser	Val	Pro	Leu	Ile	Ser	Ile	Thr	Gly	Tyr	Val	Asp	Arg	Asp	Ile	140	145	150	
Gln	Leu	Leu	Cys	Gln	Ser	Ser	Gly	Trp	Phe	Pro	Arg	Pro	Thr	Ala	155	160	165	
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Thr	Asp	Ser	Arg	170	175	180	
Thr	Asn	Arg	Asp	Met	His	Gly	Leu	Phe	Asp	Val	Glu	Ile	Ser	Leu	185	190	195	
Thr	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Ser	Cys	Ser	Met	Arg	His	200	205	210	
Ala	His	Leu	Ser	Arg	Glu	Val	Glu	Ser	Arg	Val	Gln	Ile	Gly	Asp	215	220	225	
Thr	Phe	Phe	Glu	Pro	Ile	Ser	Trp	His	Leu	Ala	Thr	Lys	Val	Leu				



<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 149  
gcgtggtcca cctctacagg gacg 24

<210> 150  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 150  
ggaactgacc cagtgtgac acc 23

<210> 151  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 151  
gcagatgcc cagtatcaag gcaggacaaa actggtgaag gattc 45

<210> 152  
<211> 2294  
<212> DNA  
<213> Homo sapiens

<400> 152  
gcgatggtgc gcccggtggc ggtggcggcg gcggttgccg aggcttcctt 50  
ggtcggattg caacgaggag aagatgactg accaaccgac tggctgaatg 100  
aatgaatggc ggagccgagc gcgccatgag gagcctgccg agcctggggc 150  
gcctcgccct gttgtgctgc gccgccgccg ccgccgccgt cgcctcagcc 200  
gcctcggcgg ggaatgtcac cgggtggcggc gggggccgcg ggcaggtgga 250  
cgcgtcgccg ggccccgggt tgcgggggcga gccagccac cccttccta 300  
ggcgacggc tcccacggc caggccccga ggaccgggccc cccgcgcgcc 350  
accgtccacc gacccttggc tgcgacttct ccagcccagt ccccgagac 400



tgttttaaga acttttagct ccttgacaaa gaagtgcitt atacttttagc 1900  
 actaaatatt ttaaagtctt tataaatgat attatactgt tatggaatat 1950  
 tgtatcatat tgtagtttat taaaaatgta gaagaggctg ggcgcggtgg 2000  
 ctcacgcctg taatcctagc actttgggag gccaaaggcg gtggatcact 2050  
 tgaggccagg agttctagat gagcctggcc agcacagtga aaccccgtct 2100  
 ctactaaaaa tacaacaaa ttagctgggc gtggtggcac acacctgtag 2150  
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 tggaggttgc agtgagctga gatcgcgcca ctgcactcca gcctggtgag 2250  
 agagggagac tctgtcttaa aaaaaaaaaa aaaaaaaaaa aaaa 2294

<210> 153  
 <211> 258  
 <212> PRT  
 <213> Homo sapiens

<400> 153  
 Met Arg Ser Leu Pro Ser Leu Gly Gly Leu Ala Leu Leu Cys Cys  
 1 5 10 15  
 Ala Ala Ala Ala Ala Val Ala Ser Ala Ala Ser Ala Gly Asn  
 20 25 30  
 Val Thr Gly Gly Gly Gly Ala Ala Gly Gln Val Asp Ala Ser Pro  
 35 40 45  
 Gly Pro Gly Leu Arg Gly Glu Pro Ser His Pro Phe Pro Arg Ala  
 50 55 60  
 Thr Ala Pro Thr Ala Gln Ala Pro Arg Thr Gly Pro Pro Arg Ala  
 65 70 75  
 Thr Val His Arg Pro Leu Ala Ala Thr Ser Pro Ala Gln Ser Pro  
 80 85 90  
 Glu Thr Thr Pro Leu Trp Ala Thr Ala Gly Pro Ser Ser Thr Thr  
 95 100 105  
 Phe Gln Ala Pro Leu Gly Pro Ser Pro Thr Thr Pro Pro Ala Ala  
 110 115 120  
 Glu Arg Thr Ser Thr Thr Ser Gln Ala Pro Thr Arg Pro Ala Pro  
 125 130 135  
 Thr Thr Leu Ser Thr Thr Thr Gly Pro Ala Pro Thr Thr Pro Val  
 140 145 150  
 Ala Thr Thr Val Pro Ala Pro Thr Thr Pro Arg Thr Pro Thr Pro  
 155 160 165  
 Asp Leu Pro Ser Ser Ser Asn Ser Ser Val Leu Pro Thr Pro Pro



	170		175		180
Ala Thr Glu Ala	Pro Ser Ser Pro Pro	Pro Glu Tyr Val Cys Asn			
	185	190			195
Cys Ser Val Val	Gly Ser Leu Asn Val	Asn Arg Cys Asn Gln Thr			
	200	205			210
Thr Gly Gln Cys	Glu Cys Arg Pro Gly	Tyr Gln Gly Leu His Cys			
	215	220			225
Glu Thr Cys Lys	Glu Gly Phe Tyr Leu	Asn Tyr Thr Ser Gly Leu			
	230	235			240
Cys Gln Pro Cys	Asp Cys Ser Pro His	Gly Ala Leu Ser Ile Pro			
	245	250			255

Cys Asn Arg

<210> 154  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 154  
 aactgctctg tgggttgaag cctg 24

<210> 155  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 155  
 cagtcacatg gctgacagac ccac 24

<210> 156  
 <211> 38  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-38  
 <223> Synthetic construct.

<400> 156  
 aggttatcag gggcttcact gtgaaacctg caaagagg 38

<210> 157  
 <211> 689  
 <212> DNA  
 <213> Homo sapiens

<400> 157  
 tgcggcgacag ttagacacgt ggaggatggg cggcctgctg ctggctgctt 50  
 ttctggcttt ggtctcggtg cccagggccc aggccgtgtg gttgggaaga 100  
 ctggaccctg agcagcttct tgggccctgg tacgtgcttg cggtggcctc 150  
 ccgggaaaag ggctttgccg tggagaagga catgaagaac gtcgtggggg 200  
 tgggtggtgac cctcactcca gaaaacaacc tgcggacgct gtcctctcag 250  
 cacgggctgg gaggggtgtga ccagagtgtc atggacctga taaagcgaaa 300  
 ctccggatgg gtgtttgaga atccctcaat aggcgtgctg gagctctggg 350  
 tgctggccac caacttcaga gactatgccg tcatcttcac tcagctggag 400  
 ttcggggacg agcccttcaa caccgtggag ctgtacagtc tgacggagac 450  
 agccagccag gagggccatgg ggctcttcac caagtggagc aggagcctgg 500  
 gcttcctgtc acagtagcag gccagctgc agaaggacct cacctgtgct 550  
 cacaagatcc ttctgtgagt gctgctgcc cagtaggat ggcgccaca 600  
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 gggccagca ccagctcaga ataaagcgat tccacagca 689

<210> 158  
 <211> 163  
 <212> PRT  
 <213> Homo sapiens

<400> 158  
 Met Gly Gly Leu Leu Leu Ala Ala Phe Leu Ala Leu Val Ser Val  
 1 5 10 15  
 Pro Arg Ala Gln Ala Val Trp Leu Gly Arg Leu Asp Pro Glu Gln  
 20 25 30  
 Leu Leu Gly Pro Trp Tyr Val Leu Ala Val Ala Ser Arg Glu Lys  
 35 40 45  
 Gly Phe Ala Met Glu Lys Asp Met Lys Asn Val Val Gly Val Val  
 50 55 60  
 Val Thr Leu Thr Pro Glu Asn Asn Leu Arg Thr Leu Ser Ser Gln  
 65 70 75  
 His Gly Leu Gly Gly Cys Asp Gln Ser Val Met Asp Leu Ile Lys  
 80 85 90

Arg	Asn	Ser	Gly	Trp	Val	Phe	Glu	Asn	Pro	Ser	Ile	Gly	Val	Leu
			95						100					105
Glu	Leu	Trp	Val	Leu	Ala	Thr	Asn	Phe	Arg	Asp	Tyr	Ala	Ile	Ile
			110						115					120
Phe	Thr	Gln	Leu	Glu	Phe	Gly	Asp	Glu	Pro	Phe	Asn	Thr	Val	Glu
			125						130					135
Leu	Tyr	Ser	Leu	Thr	Glu	Thr	Ala	Ser	Gln	Glu	Ala	Met	Gly	Leu
			140						145					150
Phe	Thr	Lys	Trp	Ser	Arg	Ser	Leu	Gly	Phe	Leu	Ser	Gln		
			155						160					

<210> 159  
 <211> 1665  
 <212> DNA  
 <213> Homo sapiens

<400> 159  
 aacagacgtt ccctgcgagg cctggcacct ctaacccag acatgctgct 50  
 gctgctgctg cccctgctct gggggagggg gagggcgga ggacagacaa 100  
 gtaaactgct gacgatgcag agttccgtga cgggtgcagga aggcctgtgt 150  
 gtccatgtgc cctgctcctt ctccctacccc tcgcatggct ggatttaccc 200  
 tggcccagta gttcatggct actggttccg ggaagggggc aatacagacc 250  
 aggatgctcc agtgccacac aacaacccag ctcgggcagt gtgggaggag 300  
 actcgggacc gattccacct ccttgggggac ccacatacca agaattgcac 350  
 cctgagcatc agagatgcca gaagaagtga tgcggggaga tacttctttc 400  
 gtatggagaa aggaagtata aaatggaatt ataaacatca ccggctctct 450  
 gtgaatgtga cagccttgac ccacaggccc aacatcctca tcccaggcac 500  
 cctggagtcc ggctgcccc agaatctgac ctgctctgtg ccctgggcct 550  
 gtgagcaggg gacaccccct atgatctcct ggataggac ctccgtgtcc 600  
 cccctggacc cctccaccac ccgctcctcg gtgctcacc tcatcccaca 650  
 gcccaggac catggcacca gcctcacctg tcagggtgacc ttccctgggg 700  
 ccagcgtgac cacgaacaag accgtccatc tcaacgtgtc ctacccgcct 750  
 cagaacttga ccatgactgt cttocaagga gacggcacag tatccacagt 800  
 cttgggaaat ggctcatctc tgctactccc agagggccag tctctgcgcc 850  
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ggtgctggag ctgccttggg tgcacctgag ggatgcagct gaattcacct 1000  
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 ctgcagagca aagccacatc aggagtgact caggggggtgg tcggggggagc 1100  
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 cctgactgaa ccttgggcag aagacagtcc cccagaccag cctccccag 1300  
 cttctgcccg ctcctcagtg ggggaaggag agctccagta tgcattccctc 1350  
 agcttcacga tggatgaagcc ttgggactcg cggggacagg aggcactga 1400  
 caccgagtac tcggagatca agatccacag atgagaaact gcagagactc 1450  
 accctgattg agggatcaca gccctccag gcaagggaga agtcagaggc 1500  
 tgattcttgt agaattaaca gccctcaacg tgatgagcta tgataaact 1550  
 atgaattatg tgcagagtga aaagcacaca ggcttttagag tcaaagtatc 1600  
 tcaaacctga atccacactg tgccctccct tttatttttt taactaaaag 1650  
 acagacaaat tccta 1665

<210> 160  
 <211> 463  
 <212> PRT  
 <213> Homo sapiens

<400> 160  
 Met Leu Leu Leu Leu Leu Pro Leu Leu Trp Gly Arg Glu Arg Ala  
 1 5 10 15  
 Glu Gly Gln Thr Ser Lys Leu Leu Thr Met Gln Ser Ser Val Thr  
 20 25 30  
 Val Gln Glu Gly Leu Cys Val His Val Pro Cys Ser Phe Ser Tyr  
 35 40 45  
 Pro Ser His Gly Trp Ile Tyr Pro Gly Pro Val Val His Gly Tyr  
 50 55 60  
 Trp Phe Arg Glu Gly Ala Asn Thr Asp Gln Asp Ala Pro Val Ala  
 65 70 75  
 Thr Asn Asn Pro Ala Arg Ala Val Trp Glu Glu Thr Arg Asp Arg  
 80 85 90  
 Phe His Leu Leu Gly Asp Pro His Thr Lys Asn Cys Thr Leu Ser  
 95 100 105  
 Ile Arg Asp Ala Arg Arg Ser Asp Ala Gly Arg Tyr Phe Phe Arg

110	115	120
Met Glu Lys Gly Ser Ile Lys Trp Asn Tyr Lys His His Arg Leu		
125	130	135
Ser Val Asn Val Thr Ala Leu Thr His Arg Pro Asn Ile Leu Ile		
140	145	150
Pro Gly Thr Leu Glu Ser Gly Cys Pro Gln Asn Leu Thr Cys Ser		
155	160	165
Val Pro Trp Ala Cys Glu Gln Gly Thr Pro Pro Met Ile Ser Trp		
170	175	180
Ile Gly Thr Ser Val Ser Pro Leu Asp Pro Ser Thr Thr Arg Ser		
185	190	195
Ser Val Leu Thr Leu Ile Pro Gln Pro Gln Asp His Gly Thr Ser		
200	205	210
Leu Thr Cys Gln Val Thr Phe Pro Gly Ala Ser Val Thr Thr Asn		
215	220	225
Lys Thr Val His Leu Asn Val Ser Tyr Pro Pro Gln Asn Leu Thr		
230	235	240
Met Thr Val Phe Gln Gly Asp Gly Thr Val Ser Thr Val Leu Gly		
245	250	255
Asn Gly Ser Ser Leu Ser Leu Pro Glu Gly Gln Ser Leu Arg Leu		
260	265	270
Val Cys Ala Val Asp Ala Val Asp Ser Asn Pro Pro Ala Arg Leu		
275	280	285
Ser Leu Ser Trp Arg Gly Leu Thr Leu Cys Pro Ser Gln Pro Ser		
290	295	300
Asn Pro Gly Val Leu Glu Leu Pro Trp Val His Leu Arg Asp Ala		
305	310	315
Ala Glu Phe Thr Cys Arg Ala Gln Asn Pro Leu Gly Ser Gln Gln		
320	325	330
Val Tyr Leu Asn Val Ser Leu Gln Ser Lys Ala Thr Ser Gly Val		
335	340	345
Thr Gln Gly Val Val Gly Gly Ala Gly Ala Thr Ala Leu Val Phe		
350	355	360
Leu Ser Phe Cys Val Ile Phe Val Val Val Arg Ser Cys Arg Lys		
365	370	375
Lys Ser Ala Arg Pro Ala Ala Gly Val Gly Asp Thr Gly Ile Glu		
380	385	390
Asp Ala Asn Ala Val Arg Gly Ser Ala Ser Gln Gly Pro Leu Thr		
395	400	405

Glu	Pro	Trp	Ala	Glu	Asp	Ser	Pro	Pro	Asp	Gln	Pro	Pro	Pro	Ala
				410					415					420
Ser	Ala	Arg	Ser	Ser	Val	Gly	Glu	Gly	Glu	Leu	Gln	Tyr	Ala	Ser
				425					430					435
Leu	Ser	Phe	Gln	Met	Val	Lys	Pro	Trp	Asp	Ser	Arg	Gly	Gln	Glu
				440					445					450
Ala	Thr	Asp	Thr	Glu	Tyr	Ser	Glu	Ile	Lys	Ile	His	Arg		
				455					460					

<210> 161  
 <211> 739  
 <212> DNA  
 <213> Homo sapiens

<400> 161  
 gacgccagtg gacctgccga ggtcggcagc acagagctct ggagatgaag 50  
 accctgttcc tgggtgtcac gctcggcctg gccgctgccc tgtccttcac 100  
 cctggaggag gaggatatca cagggacctg gtacgtgaag gccatggtgg 150  
 tcgataagga ctttcggag gacaggaggc ccaggaaggt gtccccagtg 200  
 aaggtgacag ccctgggagg tgggaagttg gaagccacgt tcaccttcac 250  
 gagggaggat cgggtgcatcc agaagaaaat cctgatgcgg aagacggagg 300  
 agcctggcaa atacagcgcc tatgggggca ggaagctcat gtacctgcag 350  
 gagctgcca ggagggacca ctacatcttt tactgcaaag accagcacca 400  
 tgggggcctg ctccacatgg gaaagcttgt gggtaggaat tctgatacca 450  
 accgggaggc cctggaagaa ttttaagaaat tgggtgcagc caagggactc 500  
 tcggaggagg acattttcac gccctgcag acgggaagct gcgttcccga 550  
 aactagga gcccccgggt ctgcacctcc agagcccacc ctaccaccag 600  
 acacagagcc cggaccacct ggacctaccc tccagccatg acccttcctt 650  
 gctcccaccc acctgactcc aaataaagtc cttttcccc aaaaaaaaaa 700  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 739

<210> 162  
 <211> 170  
 <212> PRT  
 <213> Homo sapiens

<400> 162  
 Met Lys Thr Leu Phe Leu Gly Val Thr Leu Gly Leu Ala Ala Ala  
 1 5 10 15  
 Leu Ser Phe Thr Leu Glu Glu Glu Asp Ile Thr Gly Thr Trp Tyr

20	25	30
Val Lys Ala Met Val Val Asp Lys Asp Phe Pro Glu Asp Arg Arg		
35	40	45
Pro Arg Lys Val Ser Pro Val Lys Val Thr Ala Leu Gly Gly Gly		
50	55	60
Lys Leu Glu Ala Thr Phe Thr Phe Met Arg Glu Asp Arg Cys Ile		
65	70	75
Gln Lys Lys Ile Leu Met Arg Lys Thr Glu Glu Pro Gly Lys Tyr		
80	85	90
Ser Ala Tyr Gly Gly Arg Lys Leu Met Tyr Leu Gln Glu Leu Pro		
95	100	105
Arg Arg Asp His Tyr Ile Phe Tyr Cys Lys Asp Gln His His Gly		
110	115	120
Gly Leu Leu His Met Gly Lys Leu Val Gly Arg Asn Ser Asp Thr		
125	130	135
Asn Arg Glu Ala Leu Glu Glu Phe Lys Lys Leu Val Gln Arg Lys		
140	145	150
Gly Leu Ser Glu Glu Asp Ile Phe Thr Pro Leu Gln Thr Gly Ser		
155	160	165
Cys Val Pro Glu His		
170		

<210> 163  
 <211> 22  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-22  
 <223> Synthetic construct.

<400> 163  
 ggagatgaag accctgttcc tg 22

<210> 164  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 164  
 ggagatgaag accctgttcc tgggtg 26

<210> 165  
<211> 21  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-21  
<223> Synthetic construct.

<400> 165  
gtcctccgga aagtccttat c 21

<210> 166  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 166  
gcctagtgtt cgggaacgca gcttc 25

<210> 167  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 167  
cagggacctg gtacgtgaag gccatggtgg tcgataagga ctttccggag 50

<210> 168  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 168  
ctgtccttca ccctggagga ggaggatatc acagggacct ggtac 45

<210> 169  
<211> 1204  
<212> DNA  
<213> Homo sapiens

<400> 169



gttccgcaga tgcagaggtt gaggtggctg cgggactgga agtcatcggg 50  
cagaggtctc acagcagcca aggaacctgg ggcccgtcc tccccctcc 100  
aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 150  
gtagggggag agaccaggat catcaagggg ttcgagtgc agcctcactc 200  
ccagccctgg caggcagccc tggtcgagaa gacgcggcta ctctgtgggg 250  
cgacgtcat cgccccaga tggctcctga cagcagccca ctgcctcaag 300  
ccccgctaca tagttcacct ggggcagcac aacctccaga aggaggaggg 350  
ctgtgagcag acccgagacag ccactgagtc cttccccac cccggcttca 400  
acaacagcct ccccaacaaa gaccaccgca atgacatcat gctggtgaag 450  
atggcatcgc cagtctccat cacctgggct gtgcgacccc tcacctctc 500  
ctcacgtgtg gtcactgctg gcaccagctg cctcatttcc ggctggggca 550  
gcacgtccag cccccagtta cgctgcctc acaccttgcg atgcgccaac 600  
atcaccatca ttgagcacca gaagtgtgag aacgcctacc cgggcaacat 650  
cacagacacc atggtgtgtg ccagcgtgca ggaagggggc aaggactcct 700  
gccaggggtga ctccgggggc cctctggtct gtaaccagtc tcttcaaggc 750  
attatctcct ggggccagga tccgtgtgcg atcacccgaa agcctggtgt 800  
ctacacgaaa gtctgcaa atgtggactg gatccaggag acgatgaaga 850  
acaattagac tggaccacc caccacagcc catcaccctc catttccact 900  
tggtgtttgg ttctgttca ctctgtta atgaaaccct aagccaagac 950  
cctctacgaa cattctttgg gcctcctgga ctacaggaga tgctgtcact 1000  
taataatcaa cctgggggtc gaaatcagtg agacctggat tcaaattctg 1050  
ccttgaaata ttgtgactct gggaatgaca acacctggtt tgttctctgt 1100  
tgtatcccca gcccacaaaga cagctcctgg ccatatatca aggtttcaat 1150  
aaatatttgc taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1200  
aaaa 1204

<210> 170  
<211> 250  
<212> PRT  
<213> Homo sapiens

<400> 170  
Met Arg Ile Leu Gln Leu Ile Leu Leu Ala Leu Ala Thr Gly Leu  
1 5 10 15

Val Gly Gly Glu Thr Arg Ile Ile Lys Gly Phe Glu Cys Lys Pro  
 20 25 30  
 His Ser Gln Pro Trp Gln Ala Ala Leu Phe Glu Lys Thr Arg Leu  
 35 40 45  
 Leu Cys Gly Ala Thr Leu Ile Ala Pro Arg Trp Leu Leu Thr Ala  
 50 55 60  
 Ala His Cys Leu Lys Pro Arg Tyr Ile Val His Leu Gly Gln His  
 65 70 75  
 Asn Leu Gln Lys Glu Glu Gly Cys Glu Gln Thr Arg Thr Ala Thr  
 80 85 90  
 Glu Ser Phe Pro His Pro Gly Phe Asn Asn Ser Leu Pro Asn Lys  
 95 100 105  
 Asp His Arg Asn Asp Ile Met Leu Val Lys Met Ala Ser Pro Val  
 110 115 120  
 Ser Ile Thr Trp Ala Val Arg Pro Leu Thr Leu Ser Ser Arg Cys  
 125 130 135  
 Val Thr Ala Gly Thr Ser Cys Leu Ile Ser Gly Trp Gly Ser Thr  
 140 145 150  
 Ser Ser Pro Gln Leu Arg Leu Pro His Thr Leu Arg Cys Ala Asn  
 155 160 165  
 Ile Thr Ile Ile Glu His Gln Lys Cys Glu Asn Ala Tyr Pro Gly  
 170 175 180  
 Asn Ile Thr Asp Thr Met Val Cys Ala Ser Val Gln Glu Gly Gly  
 185 190 195  
 Lys Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Asn  
 200 205 210  
 Gln Ser Leu Gln Gly Ile Ile Ser Trp Gly Gln Asp Pro Cys Ala  
 215 220 225  
 Ile Thr Arg Lys Pro Gly Val Tyr Thr Lys Val Cys Lys Tyr Val  
 230 235 240  
 Asp Trp Ile Gln Glu Thr Met Lys Asn Asn  
 245 250

<210> 171

<211> 25

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-25

<223> Synthetic construct.

<400> 171  
ggctgcggga ctggaagtca tcggg 25

<210> 172  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 172  
ctccaggcca tgaggattct gcag 24

<210> 173  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 173  
cctctggtct gtaaccag 18

<210> 174  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 174  
tctgtgatgt tgccggggta ggcg 24

<210> 175  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 175  
cgtgtagaca ccaggctttc gggtg 25

<210> 176  
<211> 18  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-18

<223> Synthetic construct.

<400> 176

cccttgatga tcctgggc 18

<210> 177

<211> 50

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-50

<223> Synthetic construct.

<400> 177

aggccatgag gattctgcag ttaatcctgc ttgctctggc aacagggctt 50

<210> 178

<211> 43

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-43

<223> Synthetic construct.

<400> 178

gagagaccag gatcatcaag gggttcgagt gcaagcctca ctc 43

<210> 179

<211> 907

<212> DNA

<213> Homo sapiens

<400> 179

gagcagtgtt ctgctggagc cgatgccaaa aaccatgcat ttcttattca 50

gattcattgt tttcttttat ctgtggggcc tttttactgc tcagagacaa 100

aagaaagagg agagcaccga agaagtgaaa atagaagttt tgcacgtcc 150

agaaaactgc tctaagacaa gcaagaaggg agacctacta aatgcccatt 200

atgacggcta cctggctaaa gacggctcga aattctactg cagccggaca 250

caaaatgaag gccaccccaa atggtttggt cttggtgttg ggcaagtcac 300

aaaaggccta gacattgcta tgacagatat gtgccctgga gaaaagcgaa 350

aagtagttat acccccttca tttgcatacg gaaaggaagg ctatgcagaa 400

ggcaagattc caccggatgc tacattgatt tttgagattg aactttatgc 450  
 tgtgacacaaa ggaccacgga gcattgagac atttaaacia atagacatgg 500  
 acaatgacag gcagctctct aaagccgaga taaacctcta cttgcaaagg 550  
 gaatttgaaa aagatgagaa gccacgtgac aagtcataatc aggatgcagt 600  
 tttagaagat atttttaaga agaatgacca tgatggtgat ggcttcattt 650  
 ctcccaagga atacaatgta taccaacacg atgaactata gcatatttgt 700  
 atttctactt ttttttttta gctatttact gtactttatg tataaaacia 750  
 agtcactttt ctccaagttg tatttgctat ttttccccta tgagaagata 800  
 ttttgatctc cccaatacat tgattttggt ataataaatg tgaggctgtt 850  
 ttgcaaactt aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 900  
 aaaaaaa 907

<210> 180  
 <211> 222  
 <212> PRT  
 <213> Homo sapiens

<400> 180  
 Met Pro Lys Thr Met His Phe Leu Phe Arg Phe Ile Val Phe Phe  
 1 5 10 15  
 Tyr Leu Trp Gly Leu Phe Thr Ala Gln Arg Gln Lys Lys Glu Glu  
 20 25 30  
 Ser Thr Glu Glu Val Lys Ile Glu Val Leu His Arg Pro Glu Asn  
 35 40 45  
 Cys Ser Lys Thr Ser Lys Lys Gly Asp Leu Leu Asn Ala His Tyr  
 50 55 60  
 Asp Gly Tyr Leu Ala Lys Asp Gly Ser Lys Phe Tyr Cys Ser Arg  
 65 70 75  
 Thr Gln Asn Glu Gly His Pro Lys Trp Phe Val Leu Gly Val Gly  
 80 85 90  
 Gln Val Ile Lys Gly Leu Asp Ile Ala Met Thr Asp Met Cys Pro  
 95 100 105  
 Gly Glu Lys Arg Lys Val Val Ile Pro Pro Ser Phe Ala Tyr Gly  
 110 115 120  
 Lys Glu Gly Tyr Ala Glu Gly Lys Ile Pro Pro Asp Ala Thr Leu  
 125 130 135  
 Ile Phe Glu Ile Glu Leu Tyr Ala Val Thr Lys Gly Pro Arg Ser  
 140 145 150

Ile Glu Thr Phe Lys Gln Ile Asp Met Asp Asn Asp Arg Gln Leu  
155 160 165

Ser Lys Ala Glu Ile Asn Leu Tyr Leu Gln Arg Glu Phe Glu Lys  
170 175 180

Asp Glu Lys Pro Arg Asp Lys Ser Tyr Gln Asp Ala Val Leu Glu  
185 190 195

Asp Ile Phe Lys Lys Asn Asp His Asp Gly Asp Gly Phe Ile Ser  
200 205 210

Pro Lys Glu Tyr Asn Val Tyr Gln His Asp Glu Leu  
215 220

<210> 181  
<211> 22  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-22  
<223> Synthetic construct.

<400> 181  
gtgttctgct ggagccgatg cc 22

<210> 182  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 182  
gacatggaca atgacagg 18

<210> 183  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 183  
cctttcagga tgtaggag 18

<210> 184  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 184  
 gatgtctgcc accccaag 18

<210> 185  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 185  
 gcatcctgat atgacttgtc acgtggc 27

<210> 186  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 186  
 tacaagaggg aagaggagtt gcac 24

<210> 187  
 <211> 52  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-52  
 <223> Synthetic construct.

<400> 187  
 gccattatg acggctacct ggctaaagac ggctcgaaat tctactgcag 50  
 cc 52

<210> 188  
 <211> 573  
 <212> DNA  
 <213> Homo sapiens

<400> 188  
 cagaaatgca gggaccattg cttcttccag gcctctgctt totgctgagc 50  
 ctctttggag ctgtgactca gaaaaccaa acttcctgtg ctaagtgcc 100

cccaaagtgt tcctgtgtca ataacactca ctgcacctgc aacctatggat 150  
 atactttctgg atctgggcag aaactattca cattccccctt ggagacatgt 200  
 aacgccaggc atggtggctc gcgcctgtaa tcccagttct ttgggaagcc 250  
 aaggcaggtg gatcacctga ggtcaggagt ttgagaccag cctggccaac 300  
 atagtgaac cccgtgtcta ctaaaaatac aaaaatcagc cgggcgtggt 350  
 ggtgcatgcc tgcaatccca gttactcggg aggctgaggc aggagaatcg 400  
 cttgaactca ggaggcagaa gttgcagtga acccagatcc tgccattgca 450  
 ctccagcatg gatgacagag caagactccg tctcaaaaag aaaagatagt 500  
 ttcttgtttc atttcgagac tgccctctca gtgtttcctg ggatcccctc 550  
 ccaaataaag tacttatatt ctc 573

<210> 189  
 <211> 74  
 <212> PRT  
 <213> Homo sapiens

<400> 189  
 Met Gln Gly Pro Leu Leu Leu Pro Gly Leu Cys Phe Leu Leu Ser  
 1 5 10 15  
 Leu Phe Gly Ala Val Thr Gln Lys Thr Lys Thr Ser Cys Ala Lys  
 20 25 30  
 Cys Pro Pro Asn Ala Ser Cys Val Asn Asn Thr His Cys Thr Cys  
 35 40 45  
 Asn His Gly Tyr Thr Ser Gly Ser Gly Gln Lys Leu Phe Thr Phe  
 50 55 60  
 Pro Leu Glu Thr Cys Asn Ala Arg His Gly Gly Ser Arg Leu  
 65 70

<210> 190  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 190  
 aggaccatt gcttcttcca ggcc 24

<210> 191  
 <211> 24  
 <212> DNA  
 <213> Artificial



<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 191  
 cgttacatgt ctccaagggg aatg 24

<210> 192  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 192  
 cctgtgctaa gtgcccccca aatgcttcct gtgtcaataa cactcactgc 50

<210> 193  
 <211> 1091  
 <212> DNA  
 <213> Homo sapiens

<400> 193  
 caagcagggtc atcccccttgg tgaccttcaa agagaagcag agagggcaga 50  
 ggtgggggggc acagggaaag ggtgacctct gagattcccc ttttccccca 100  
 gactttggaa gtgaccaccc atgggggtca gcatcttttt gctcctgtgt 150  
 gttcttgggc tcagccaggc agccacaccg aagattttca atggcactga 200  
 gtgtgggcgt aactcacagc cgtggcaggt ggggctgttt gagggcacca 250  
 gcctgcgctg cgggggtgtc cttattgacc acaggtgggt cctcacagcg 300  
 gctcactgca gcggcagcag gtactgggtg cgcttggggg aacacagcct 350  
 cagccagctc gactggaccg agcagatccg gcacagcggc ttctctgtga 400  
 cccatcccgg ctacctggga gcctcgacga gccacgagca cgacctccgg 450  
 ctgctgcggc tgcgcctgcc cgtccgcgta accagcagcg ttcaaccct 500  
 gccctgccc aatgactgtg caacogctgg caccgagtgc cacgtctcag 550  
 gctggggcat caccaaccac ccacggaacc cattcccga tctgctccag 600  
 tgctcaacc tctccatcgt ctcccatgcc acctgccatg gtgtgtatcc 650  
 cgggagaatc acgagcaaca tgggtgtgtg agggggcgtc ccggggcagg 700  
 atgcctgcca ggggtgattct gggggccccc tgggtgtgtg gggagtcctt 750  
 caaggtctgg tgtcctgggg gtctgtgggg ccctgtggac aagatggcat 800

ccctggagtc tacacctata ttgcaagta tgtggactgg atccggatga 850  
 tcatgaggaa caactgacct gtttctcca cctccacccc cacccttaa 900  
 cttgggtacc cctctggccc tcagagcacc aatatctcct ccatcacttc 950  
 ccctagctcc actcttggtg gcctgggaac ttcttgggaac ttttaactcct 1000  
 gccagccctt ctaagaccca cgagcgggggt gagagaagtg tgcaatagtc 1050  
 tggaataaat ataatgaag gaggggcaaa aaaaaaaaaa a 1091

<210> 194  
 <211> 248  
 <212> PRT  
 <213> Homo sapiens

<400> 194  
 Met Gly Leu Ser Ile Phe Leu Leu Leu Cys Val Leu Gly Leu Ser  
     1                    5                    10                    15  
 Gln Ala Ala Thr Pro Lys Ile Phe Asn Gly Thr Glu Cys Gly Arg  
                     20                    25                    30  
 Asn Ser Gln Pro Trp Gln Val Gly Leu Phe Glu Gly Thr Ser Leu  
                     35                    40                    45  
 Arg Cys Gly Gly Val Leu Ile Asp His Arg Trp Val Leu Thr Ala  
                     50                    55                    60  
 Ala His Cys Ser Gly Ser Arg Tyr Trp Val Arg Leu Gly Glu His  
                     65                    70                    75  
 Ser Leu Ser Gln Leu Asp Trp Thr Glu Gln Ile Arg His Ser Gly  
                     80                    85                    90  
 Phe Ser Val Thr His Pro Gly Tyr Leu Gly Ala Ser Thr Ser His  
                     95                    100                    105  
 Glu His Asp Leu Arg Leu Leu Arg Leu Arg Leu Pro Val Arg Val  
                     110                    115                    120  
 Thr Ser Ser Val Gln Pro Leu Pro Leu Pro Asn Asp Cys Ala Thr  
                     125                    130                    135  
 Ala Gly Thr Glu Cys His Val Ser Gly Trp Gly Ile Thr Asn His  
                     140                    145                    150  
 Pro Arg Asn Pro Phe Pro Asp Leu Leu Gln Cys Leu Asn Leu Ser  
                     155                    160                    165  
 Ile Val Ser His Ala Thr Cys His Gly Val Tyr Pro Gly Arg Ile  
                     170                    175                    180  
 Thr Ser Asn Met Val Cys Ala Gly Gly Val Pro Gly Gln Asp Ala  
                     185                    190                    195  
 Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Cys Gly Gly Val Leu

	200		205		210
Gln Gly Leu Val Ser Trp Gly Ser Val Gly Pro Cys Gly Gln Asp					
	215		220		225
Gly Ile Pro Gly Val Tyr Thr Tyr Ile Cys Lys Tyr Val Asp Trp					
	230		235		240
Ile Arg Met Ile Met Arg Asn Asn					
	245				

<210> 195  
 <211> 1485  
 <212> DNA  
 <213> Homo sapiens

<400> 195  
 gcggccacac gcagctagcc ggagcccgga ccaggcgcct gtgcctcctc 50  
 ctcgtccctc gccgcgtccg cgaagcctgg agccggcggg agccccgcgc 100  
 tcgccatgtc gggcgagctc agcaacaggt tccaaggagg gaaggcgttc 150  
 ggcttgctca aagcccggca ggagaggagg ctggccgaga tcaaccggga 200  
 gtttctgtgt gaccagaagt acagtgatga agagaacctt ccagaaaagc 250  
 tcacagcctt caaagagaag tacatggagt ttgacctgaa caatgaaggc 300  
 gagattgacc tgatgtcttt aaagaggatg atggagaagc ttggtgtccc 350  
 caagaccac ctggagatga agaagatgat ctgagagggt acaggagggg 400  
 tcagtgcac tatatcctac cgagactttg tgaacatgat gctggggaaa 450  
 cggtcggctg tcctcaagtt agtcatgatg tttgaaggaa aagccaacga 500  
 gagcagcccc aagccagttg gccccctcc agagagagac attgctagcc 550  
 tgccctgagg accccgcctg gactccccag ccttcccacc ccatacctcc 600  
 ctcccgatct tgctgccctt cttgacacac tgtgatctct ctctctctca 650  
 tttgtttggt cattgagggg ttgtttgtgt tttcatcaat gtctttgtaa 700  
 agcaciaaatt atctgcctta aaggggctct gggtcgggga atcctgagcc 750  
 ttgggtcccc tccctctctt cttccctcct tccccgctcc ctgtgcagaa 800  
 gggctgatat caaaccaaaa actagagggg gcagggccag ggcaggagg 850  
 cttccagcct gtgttccccct cacttgaggg aaccagcact ctccatcctt 900  
 tcagaaagtc tccaagccaa gttcaggctc actgacctgg ctctgacgag 950  
 gacccaggc cactctgaga agaccttgga gtagggacaa ggctgcaggg 1000  
 cctctttcgg gtttccttgg acagtgccat ggttccagtg ctctggtgtc 1050

acccaggaca cagccactcg gggccccgct gccccagctg atccccactc 1100  
 attccacacc tcttctcatc ctcaagtatg tgaaggtggg aaggaaagga 1150  
 gcttggcatt gggagccctt caagaaggta ccagaaggaa ccctccagtc 1200  
 ctgctctctg gccacacctg tgcaggcagc tgagaggcag cgtgcagccc 1250  
 tactgtccct tactggggca gcagagggct tcggaggcag aagtgaggcc 1300  
 tggggtttgg ggggaaaggt cagctcagtg ctgttccacc ttttagggag 1350  
 gatactgagg ggaccaggat gggagaatga ggagtaaaat gctcacggca 1400  
 aagtcagcag cactggtaag ccaagactga gaaatacaag gttgcttgtc 1450  
 tgaccccaat ctgcttgaaa aaaaaaaaaa aaaaa 1485

<210> 196  
 <211> 150  
 <212> PRT  
 <213> Homo sapiens

<400> 196  
 Met Ser Gly Glu Leu Ser Asn Arg Phe Gln Gly Gly Lys Ala Phe  
 1 5 10 15  
 Gly Leu Leu Lys Ala Arg Gln Glu Arg Arg Leu Ala Glu Ile Asn  
 20 25 30  
 Arg Glu Phe Leu Cys Asp Gln Lys Tyr Ser Asp Glu Glu Asn Leu  
 35 40 45  
 Pro Glu Lys Leu Thr Ala Phe Lys Glu Lys Tyr Met Glu Phe Asp  
 50 55 60  
 Leu Asn Asn Glu Gly Glu Ile Asp Leu Met Ser Leu Lys Arg Met  
 65 70 75  
 Met Glu Lys Leu Gly Val Pro Lys Thr His Leu Glu Met Lys Lys  
 80 85 90  
 Met Ile Ser Glu Val Thr Gly Gly Val Ser Asp Thr Ile Ser Tyr  
 95 100 105  
 Arg Asp Phe Val Asn Met Met Leu Gly Lys Arg Ser Ala Val Leu  
 110 115 120  
 Lys Leu Val Met Met Phe Glu Gly Lys Ala Asn Glu Ser Ser Pro  
 125 130 135  
 Lys Pro Val Gly Pro Pro Pro Glu Arg Asp Ile Ala Ser Leu Pro  
 140 145 150

<210> 197  
 <211> 4842  
 <212> DNA  
 <213> Homo sapiens

&lt;400&gt; 197

cgcgctcccc gcgcgcctcc tcggggtcca cgcgctttgc cccgcagagg 50  
 cagcctcctc caggagcggg gccctgcaca ccatggcccc cgggtgggca 100  
 ggggtcggcg ccgccgtgcg cgcccgcctg gcgctggcct tggcgctggc 150  
 gagcgtcctg agtgggcctc cagccgtcgc ctgccccacc aagtgtacct 200  
 gctccgctgc cagcgtggac tgccacgggc tgggcctccg cgcggttcc 250  
 cggggcatcc cccgcaacgc tgagcgcctt gacctggaca gaaataatat 300  
 caccaggatc accaagatgg acttcgctgg gctcaagaac ctccgagtct 350  
 tgcattctgga agacaaccag gtcagcgtca tcgagagagg cgccttccag 400  
 gacctgaagc agctagagcg actgcgcctg aacaagaata agctgcaagt 450  
 ccttccagaa ttgcttttcc agagcacgcc gaagctcacc agactagatt 500  
 tgagtgaana ccagatccag gggatcccg ggaaggcgtt ccgcggcatc 550  
 accgatgtga agaacctgca actggacaac aaccacatca gctgcattga 600  
 agatggagcc ttccgagcgc tgcgcgattt ggagatcctt accctcaaca 650  
 acaacaacat cagtcgcac cttgtcacca gcttcaacca catgccgaag 700  
 atccgaactc tgcgcctcca ctccaaccac ctctactgcg actgccacct 750  
 ggcctggctc tcggattggc tgcgacagcg acggacagtt ggccagttca 800  
 cactctgcat ggctcctgtg catttgaggg gcttcaacgt ggcggatgtg 850  
 cagaagaagg agtaogtgtg cccagcccc cactcggagc ccccatcctg 900  
 caatgccaac tccatctcct gcccttcgcc ctgcacgtgc agcaataaca 950  
 tcgtggactg tcgaggaaag ggcttgatgg agattcctgc caacttgccg 1000  
 gagggcatcg tcgaaatacg cctagaacag aactccatca aagccatccc 1050  
 tgcaggagcc ttcaccagct acaagaaact gaagcgaata gacatcagca 1100  
 agaatcagat atcgatatt gctccagatg ccttccaggg cctgaaatca 1150  
 ctacatcgc tggctcctgta tgggaacaag atcaccgaga ttgccaaggg 1200  
 actgtttgat gggctgggtg ccctacagct gctcctcctc aatgccaaca 1250  
 agatcaactg cctgcgggtg aacacgtttc aggacctgca gaacctcaac 1300  
 ttgctctccc tgtatgacaa caagctgcag accatcagca aggggtctct 1350  
 cgcccctctg cagtccatcc agacactcca cttagcccaa aaccatttg 1400  
 tgtgcgactg ccaattgaag tggctggccg actacctcca ggacaacccc 1450





catctcagac caaggggagc cctactgcct gtgccagccc ggcttttagcg 4400  
 gcgagcactg ccaacaagag aatccgtgcc tgggacaagt agtccgagag 4450  
 gtgatccgcc gccagaaagg ttatgcatca tgtgccacag cctccaaggt 4500  
 gcccatcatg gaatgtcgtg ggggctgtgg gccccagtgc tgccagccca 4550  
 cccgcagcaa gcggcggaac tacgtcttcc agtgcacgga cggctcctcg 4600  
 tttgtagaag aggtggagag acacttagag tgcggctgcc tcgctgttgc 4650  
 ctaagcccct gcccgctgc ctgccacctc tcggactcca gcttgatgga 4700  
 gttgggacag ccatgtggga cccctgtgtg attcagcatg aaggaaatga 4750  
 agctggagag gaaggtaaag aagaagagaa tattaagtat attgtaaaat 4800  
 aaacaaaaaa tagaacttaa aaaaaaaaaa aaaaaaaaaa aa 4842

<210> 198  
 <211> 1523  
 <212> PRT  
 <213> Homo sapiens

<400> 198  
 Met Ala Pro Gly Trp Ala Gly Val Gly Ala Ala Val Arg Ala Arg  
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 Leu Ala Leu Ala Leu Ala Leu Ala Ser Val Leu Ser Gly Pro Pro  
 20 25 30  
 Ala Val Ala Cys Pro Thr Lys Cys Thr Cys Ser Ala Ala Ser Val  
 35 40 45  
 Asp Cys His Gly Leu Gly Leu Arg Ala Val Pro Arg Gly Ile Pro  
 50 55 60  
 Arg Asn Ala Glu Arg Leu Asp Leu Asp Arg Asn Asn Ile Thr Arg  
 65 70 75  
 Ile Thr Lys Met Asp Phe Ala Gly Leu Lys Asn Leu Arg Val Leu  
 80 85 90  
 His Leu Glu Asp Asn Gln Val Ser Val Ile Glu Arg Gly Ala Phe  
 95 100 105  
 Gln Asp Leu Lys Gln Leu Glu Arg Leu Arg Leu Asn Lys Asn Lys  
 110 115 120  
 Leu Gln Val Leu Pro Glu Leu Leu Phe Gln Ser Thr Pro Lys Leu  
 125 130 135  
 Thr Arg Leu Asp Leu Ser Glu Asn Gln Ile Gln Gly Ile Pro Arg  
 140 145 150  
 Lys Ala Phe Arg Gly Ile Thr Asp Val Lys Asn Leu Gln Leu Asp  
 155 160 165



Asn Asn His Ile	Ser Cys Ile Glu Asp	Gly Ala Phe Arg Ala	Leu
170		175	180
Arg Asp Leu Glu	Ile Leu Thr Leu Asn	Asn Asn Asn Ile Ser	Arg
185		190	195
Ile Leu Val Thr	Ser Phe Asn His Met	Pro Lys Ile Arg Thr	Leu
200		205	210
Arg Leu His Ser	Asn His Leu Tyr Cys	Asp Cys His Leu Ala	Trp
215		220	225
Leu Ser Asp Trp	Leu Arg Gln Arg Arg	Thr Val Gly Gln Phe	Thr
230		235	240
Leu Cys Met Ala	Pro Val His Leu Arg	Gly Phe Asn Val Ala	Asp
245		250	255
Val Gln Lys Lys	Glu Tyr Val Cys Pro	Ala Pro His Ser Glu	Pro
260		265	270
Pro Ser Cys Asn	Ala Asn Ser Ile Ser	Cys Pro Ser Pro Cys	Thr
275		280	285
Cys Ser Asn Asn	Ile Val Asp Cys Arg	Gly Lys Gly Leu Met	Glu
290		295	300
Ile Pro Ala Asn	Leu Pro Glu Gly Ile	Val Glu Ile Arg Leu	Glu
305		310	315
Gln Asn Ser Ile	Lys Ala Ile Pro Ala	Gly Ala Phe Thr Gln	Tyr
320		325	330
Lys Lys Leu Lys	Arg Ile Asp Ile Ser	Lys Asn Gln Ile Ser	Asp
335		340	345
Ile Ala Pro Asp	Ala Phe Gln Gly Leu	Lys Ser Leu Thr Ser	Leu
350		355	360
Val Leu Tyr Gly	Asn Lys Ile Thr Glu	Ile Ala Lys Gly Leu	Phe
365		370	375
Asp Gly Leu Val	Ser Leu Gln Leu Leu	Leu Leu Asn Ala Asn	Lys
380		385	390
Ile Asn Cys Leu	Arg Val Asn Thr Phe	Gln Asp Leu Gln Asn	Leu
395		400	405
Asn Leu Leu Ser	Leu Tyr Asp Asn Lys	Leu Gln Thr Ile Ser	Lys
410		415	420
Gly Leu Phe Ala	Pro Leu Gln Ser Ile	Gln Thr Leu His Leu	Ala
425		430	435
Gln Asn Pro Phe	Val Cys Asp Cys His	Leu Lys Trp Leu Ala	Asp
440		445	450
Tyr Leu Gln Asp	Asn Pro Ile Glu Thr	Ser Gly Ala Arg Cys	Ser

	455		460		465
Ser Pro Arg Arg	Leu Ala Asn Lys Arg	Ile Ser Gln Ile Lys Ser			
	470	475			480
Lys Lys Phe Arg	Cys Ser Gly Ser Glu Asp Tyr Arg Ser Arg	Phe			
	485	490			495
Ser Ser Glu Cys	Phe Met Asp Leu Val	Cys Pro Glu Lys Cys Arg			
	500	505			510
Cys Glu Gly Thr	Ile Val Asp Cys Ser	Asn Gln Lys Leu Val Arg			
	515	520			525
Ile Pro Ser His	Leu Pro Glu Tyr Val	Thr Asp Leu Arg Leu Asn			
	530	535			540
Asp Asn Glu Val	Ser Val Leu Glu Ala	Thr Gly Ile Phe Lys Lys			
	545	550			555
Leu Pro Asn Leu	Arg Lys Ile Asn Leu	Ser Asn Asn Lys Ile Lys			
	560	565			570
Glu Val Arg Glu	Gly Ala Phe Asp Gly	Ala Ala Ser Val Gln Glu			
	575	580			585
Leu Met Leu Thr	Gly Asn Gln Leu Glu	Thr Val His Gly Arg Val			
	590	595			600
Phe Arg Gly Leu	Ser Gly Leu Lys Thr	Leu Met Leu Arg Ser Asn			
	605	610			615
Leu Ile Ser Cys	Val Ser Asn Asp Thr	Phe Ala Gly Leu Ser Ser			
	620	625			630
Val Arg Leu Leu	Ser Leu Tyr Asp Asn	Arg Ile Thr Thr Ile Thr			
	635	640			645
Pro Gly Ala Phe	Thr Thr Leu Val Ser	Leu Ser Thr Ile Asn Leu			
	650	655			660
Leu Ser Asn Pro	Phe Asn Cys Asn Cys	His Leu Ala Trp Leu Gly			
	665	670			675
Lys Trp Leu Arg	Lys Arg Arg Ile Val	Ser Gly Asn Pro Arg Cys			
	680	685			690
Gln Lys Pro Phe	Phe Leu Lys Glu Ile	Pro Ile Gln Asp Val Ala			
	695	700			705
Ile Gln Asp Phe	Thr Cys Asp Gly Asn	Glu Glu Ser Ser Cys Gln			
	710	715			720
Leu Ser Pro Arg	Cys Pro Glu Gln Cys	Thr Cys Met Glu Thr Val			
	725	730			735
Val Arg Cys Ser	Asn Lys Gly Leu Arg	Ala Leu Pro Arg Gly Met			
	740	745			750

Pro Lys Asp Val	Thr Glu Leu Tyr Leu	Glu Gly Asn His Leu	Thr
	755	760	765
Ala Val Pro Arg	Glu Leu Ser Ala Leu	Arg His Leu Thr Leu	Ile
	770	775	780
Asp Leu Ser Asn	Asn Ser Ile Ser Met	Leu Thr Asn Tyr Thr	Phe
	785	790	795
Ser Asn Met Ser	His Leu Ser Thr Leu	Ile Leu Ser Tyr Asn	Arg
	800	805	810
Leu Arg Cys Ile	Pro Val His Ala Phe	Asn Gly Leu Arg Ser	Leu
	815	820	825
Arg Val Leu Thr	Leu His Gly Asn Asp	Ile Ser Ser Val Pro	Glu
	830	835	840
Gly Ser Phe Asn	Asp Leu Thr Ser Leu	Ser His Leu Ala Leu	Gly
	845	850	855
Thr Asn Pro Leu	His Cys Asp Cys Ser	Leu Arg Trp Leu Ser	Glu
	860	865	870
Trp Val Lys Ala	Gly Tyr Lys Glu Pro	Gly Ile Ala Arg Cys	Ser
	875	880	885
Ser Pro Glu Pro	Met Ala Asp Arg Leu	Leu Leu Thr Thr Pro	Thr
	890	895	900
His Arg Phe Gln	Cys Lys Gly Pro Val	Asp Ile Asn Ile Val	Ala
	905	910	915
Lys Cys Asn Ala	Cys Leu Ser Ser Pro	Cys Lys Asn Asn Gly	Thr
	920	925	930
Cys Thr Gln Asp	Pro Val Glu Leu Tyr	Arg Cys Ala Cys Pro	Tyr
	935	940	945
Ser Tyr Lys Gly	Lys Asp Cys Thr Val	Pro Ile Asn Thr Cys	Ile
	950	955	960
Gln Asn Pro Cys	Gln His Gly Gly Thr	Cys His Leu Ser Asp	Ser
	965	970	975
His Lys Asp Gly	Phe Ser Cys Ser Cys	Pro Leu Gly Phe Glu	Gly
	980	985	990
Gln Arg Cys Glu	Ile Asn Pro Asp Asp	Cys Glu Asp Asn Asp	Cys
	995	1000	1005
Glu Asn Asn Ala	Thr Cys Val Asp Gly	Ile Asn Asn Tyr Val	Cys
	1010	1015	1020
Ile Cys Pro Pro	Asn Tyr Thr Gly Glu	Leu Cys Asp Glu Val	Ile
	1025	1030	1035
Asp His Cys Val	Pro Glu Leu Asn Leu	Cys Gln His Glu Ala	Lys

1040	1045	1050
Cys Ile Pro Leu Asp 1055	Lys Gly Phe Ser Cys Glu Cys Val Pro Gly 1060	1065
Tyr Ser Gly Lys Leu Cys Glu Thr Asp Asn Asp Asp Cys Val Ala 1070	1075	1080
His Lys Cys Arg His Gly Ala Gln Cys Val Asp Thr Ile Asn Gly 1085	1090	1095
Tyr Thr Cys Thr Cys Pro Gln Gly Phe Ser Gly Pro Phe Cys Glu 1100	1105	1110
His Pro Pro Pro Met Val Leu Leu Gln Thr Ser Pro Cys Asp Gln 1115	1120	1125
Tyr Glu Cys Gln Asn Gly Ala Gln Cys Ile Val Val Gln Gln Glu 1130	1135	1140
Pro Thr Cys Arg Cys Pro Pro Gly Phe Ala Gly Pro Arg Cys Glu 1145	1150	1155
Lys Leu Ile Thr Val Asn Phe Val Gly Lys Asp Ser Tyr Val Glu 1160	1165	1170
Leu Ala Ser Ala Lys Val Arg Pro Gln Ala Asn Ile Ser Leu Gln 1175	1180	1185
Val Ala Thr Asp Lys Asp Asn Gly Ile Leu Leu Tyr Lys Gly Asp 1190	1195	1200
Asn Asp Pro Leu Ala Leu Glu Leu Tyr Gln Gly His Val Arg Leu 1205	1210	1215
Val Tyr Asp Ser Leu Ser Ser Pro Pro Thr Thr Val Tyr Ser Val 1220	1225	1230
Glu Thr Val Asn Asp Gly Gln Phe His Ser Val Glu Leu Val Thr 1235	1240	1245
Leu Asn Gln Thr Leu Asn Leu Val Val Asp Lys Gly Thr Pro Lys 1250	1255	1260
Ser Leu Gly Lys Leu Gln Lys Gln Pro Ala Val Gly Ile Asn Ser 1265	1270	1275
Pro Leu Tyr Leu Gly Gly Ile Pro Thr Ser Thr Gly Leu Ser Ala 1280	1285	1290
Leu Arg Gln Gly Thr Asp Arg Pro Leu Gly Gly Phe His Gly Cys 1295	1300	1305
Ile His Glu Val Arg Ile Asn Asn Glu Leu Gln Asp Phe Lys Ala 1310	1315	1320
Leu Pro Pro Gln Ser Leu Gly Val Ser Pro Gly Cys Lys Ser Cys 1325	1330	1335

Thr Val Cys Lys His Gly Leu Cys Arg Ser Val Glu Lys Asp Ser  
1340 1345 1350

Val Val Cys Glu Cys Arg Pro Gly Trp Thr Gly Pro Leu Cys Asp  
1355 1360 1365

Gln Glu Ala Arg Asp Pro Cys Leu Gly His Arg Cys His His Gly  
1370 1375 1380

Lys Cys Val Ala Thr Gly Thr Ser Tyr Met Cys Lys Cys Ala Glu  
1385 1390 1395

Gly Tyr Gly Gly Asp Leu Cys Asp Asn Lys Asn Asp Ser Ala Asn  
1400 1405 1410

Ala Cys Ser Ala Phe Lys Cys His His Gly Gln Cys His Ile Ser  
1415 1420 1425

Asp Gln Gly Glu Pro Tyr Cys Leu Cys Gln Pro Gly Phe Ser Gly  
1430 1435 1440

Glu His Cys Gln Gln Glu Asn Pro Cys Leu Gly Gln Val Val Arg  
1445 1450 1455

Glu Val Ile Arg Arg Gln Lys Gly Tyr Ala Ser Cys Ala Thr Ala  
1460 1465 1470

Ser Lys Val Pro Ile Met Glu Cys Arg Gly Gly Cys Gly Pro Gln  
1475 1480 1485

Cys Cys Gln Pro Thr Arg Ser Lys Arg Arg Lys Tyr Val Phe Gln  
1490 1495 1500

Cys Thr Asp Gly Ser Ser Phe Val Glu Glu Val Glu Arg His Leu  
1505 1510 1515

Glu Cys Gly Cys Leu Ala Cys Ser  
1520

<210> 199

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic construct.

<400> 199

atggagattc ctgccaaactt gccg 24

<210> 200

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 200  
ttgttgcat tgaggaggag cagc 24

<210> 201  
<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 201  
gagggcatcg tcgaaatagc cctagaacag aactccatca aagccatccc 50

<210> 202  
<211> 753  
<212> DNA  
<213> Homo sapiens

<400> 202  
ggatgcagga cgctcccctg agctgcctgt caccgactag gtggagcagt 50  
gtttcttccg cagactcaac tgagaagtca gcctctgggg caggcaccag 100  
gaatctgcct tttagttct gtctccggca ggctttgagg atgaaggctg 150  
cgggcattct gaccctcatt ggctgcctgg tcacaggcgc cgagtccaaa 200  
atctacactc gttgcaaact ggcaaaaata ttctcgaggg ctggcctgga 250  
caattactgg ggcttcagcc ttggaaactg gatctgcatg gcatattatg 300  
agagoggcta caacaccaca gccccgacgg tcctggatga cggcagcatc 350  
gactatggca tcttcagat caacagcttc gcgtggtgca gacgcggaaa 400  
gctgaaggag aacaaccact gccatgtcgc ctgctcagcc ttgatcactg 450  
atgacctcac agatgcaatt atctgtgccg ggaaaattgt taaagagaca 500  
caaggaatga actattggca aggctggaag aaacattgtg agggcagaga 550  
cctgtccgag tggaaaaaag gctgtgaggt ttcctaaact ggaactggac 600  
ccaggatgct ttgcagcaac gccctaggat ttgcagtga tgtccaaatg 650  
cctgtgtcat cttgtcccgt ttcctcccaa tattccttct caaacttggg 700  
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gtc 753

<210> 203  
 <211> 148  
 <212> PRT  
 <213> Homo sapiens

<400> 203  
 Met Lys Ala Ala Gly Ile Leu Thr Leu Ile Gly Cys Leu Val Thr  
 1 5 10 15  
 Gly Ala Glu Ser Lys Ile Tyr Thr Arg Cys Lys Leu Ala Lys Ile  
 20 25 30  
 Phe Ser Arg Ala Gly Leu Asp Asn Tyr Trp Gly Phe Ser Leu Gly  
 35 40 45  
 Asn Trp Ile Cys Met Ala Tyr Tyr Glu Ser Gly Tyr Asn Thr Thr  
 50 55 60  
 Ala Pro Thr Val Leu Asp Asp Gly Ser Ile Asp Tyr Gly Ile Phe  
 65 70 75  
 Gln Ile Asn Ser Phe Ala Trp Cys Arg Arg Gly Lys Leu Lys Glu  
 80 85 90  
 Asn Asn His Cys His Val Ala Cys Ser Ala Leu Ile Thr Asp Asp  
 95 100 105  
 Leu Thr Asp Ala Ile Ile Cys Ala Arg Lys Ile Val Lys Glu Thr  
 110 115 120  
 Gln Gly Met Asn Tyr Trp Gln Gly Trp Lys Lys His Cys Glu Gly  
 125 130 135  
 Arg Asp Leu Ser Glu Trp Lys Lys Gly Cys Glu Val Ser  
 140 145

<210> 204  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 204  
 gcaggctttg aggatgaagg ctgc 24

<210> 205  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 205  
ctcattggct gcctggtcac aggc 24

<210> 206  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 206  
ccagtcggac aggtctctcc cctc 24

<210> 207  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 207  
tcagtgacca aggctgagca ggcg 24

<210> 208  
<211> 47  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 208  
ctacactcgt tgcaaaactgg caaaaatatt ctcgagggtt ggcctgg 47

<210> 209  
<211> 1648  
<212> DNA  
<213> Homo sapiens

<400> 209  
caggccatatt gcatccact gtccttgtgt tcggagccag gccacaccgt 50  
cctcagcagt gtcattgtgt aaaaacgcca agctgaatat atcatgcccc 100  
tattaaaaact tgtacatggc tccccattgg tttttggaga aaagttcaag 150  
ctttttacct tgggtgtctgc ctgtatccca gtgttcaggc tggctagacg 200  
gcggaagaag atcctatatt actgtcactt cccagatctg cttctcacca 250



agagagattc ttttcttaaa cgactataca gggccccaat tgactggata 300  
gaggaatata ccacaggcat ggcagactgc atcttagtca acagccagtt 350  
cacagctgct gtttttaagg aaacattcaa gtccctgtct cacatagacc 400  
ctgatgtcct ctatccatct ctaaagtgtca ccagctttga ctcagttggt 450  
cctgaaaagc tggatgacct agtccccaag gggaaaaaat tcctgctgct 500  
ctccatcaac agatacgaaa ggaagaaaaa tctgactttg gcactggaag 550  
ccctagtaca gctgcgtgga agattgacat cccaagattg ggagaggggt 600  
catctgatcg tggcaggtgg ttatgacgag agagtccctgg agaattgtgga 650  
acattatcag gaattgaaga aaatgggtcca acagtccgac cttggccagt 700  
atgtgacctt cttgaggtct ttctcagaca aacagaaaaat ctccctcctc 750  
cacagctgca cgtgtgtgct ttacacacca agcaatgagc actttggcat 800  
tgtccctctg gaagccatgt acatgcagtg cccagtcatt gctgttaatt 850  
cgggtggacc cttggagtc attgaccaca gtgtcacagg gtttctgtgt 900  
gagcctgacc cgggtgcactt ctcagaagca atagaaaagt tcatccgtga 950  
accttcctta aaagccacca tgggcctggc tggaagagcc agagtgaagg 1000  
aaaaattttc ccctgaagca ttacagaac agctctaccg atatgttacc 1050  
aaactgctgg tataatcaga ttgtttttta gatctccatt aatgtcattt 1100  
ttatggattg tagaaccagt tttgaaacca aaaaagaaac ctagaatcta 1150  
atgcagaaga gatcttttaa aaaataaact tgagtcttga atgtgagcca 1200  
ctttcctata taccacacct ccctgtccac ttttcagaaa aaccatgtct 1250  
tttatgctat aatcattcca aattttgcca gtgttaagtt acaaattgtg 1300  
tgtcattcca tgttcagcag agtattttaa ttatatatttc tcgggattat 1350  
tgctcttctg tctataaatt ttgaatgata ctgtgcctta attggttttc 1400  
atagtttaag tgtgtatcat tatcaaagtt gattaatttg gcttcatagt 1450  
ataatgagag cagggtctatt gtagttccca gattcaatcc accgaagtgt 1500  
tactgtcat ctgttaggga atttttgttt gtccctgtctt tgccctggatc 1550  
catagcgaga gtgctctgta ttttttttaa gataatttgt atttttgcac 1600  
actgagatat aataaaaggt gtttatcata aaaaaaaaaa aaaaaaaa 1648

<210> 210  
<211> 323

<212> PRT  
 <213> Homo sapiens

<400> 210

Met	Pro	Leu	Leu	Lys	Leu	Val	His	Gly	Ser	Pro	Leu	Val	Phe	Gly	1	5	10	15
Glu	Lys	Phe	Lys	Leu	Phe	Thr	Leu	Val	Ser	Ala	Cys	Ile	Pro	Val	20	25	30	
Phe	Arg	Leu	Ala	Arg	Arg	Arg	Lys	Lys	Ile	Leu	Phe	Tyr	Cys	His	35	40	45	
Phe	Pro	Asp	Leu	Leu	Leu	Thr	Lys	Arg	Asp	Ser	Phe	Leu	Lys	Arg	50	55	60	
Leu	Tyr	Arg	Ala	Pro	Ile	Asp	Trp	Ile	Glu	Glu	Tyr	Thr	Thr	Gly	65	70	75	
Met	Ala	Asp	Cys	Ile	Leu	Val	Asn	Ser	Gln	Phe	Thr	Ala	Ala	Val	80	85	90	
Phe	Lys	Glu	Thr	Phe	Lys	Ser	Leu	Ser	His	Ile	Asp	Pro	Asp	Val	95	100	105	
Leu	Tyr	Pro	Ser	Leu	Asn	Val	Thr	Ser	Phe	Asp	Ser	Val	Val	Pro	110	115	120	
Glu	Lys	Leu	Asp	Asp	Leu	Val	Pro	Lys	Gly	Lys	Lys	Phe	Leu	Leu	125	130	135	
Leu	Ser	Ile	Asn	Arg	Tyr	Glu	Arg	Lys	Lys	Asn	Leu	Thr	Leu	Ala	140	145	150	
Leu	Glu	Ala	Leu	Val	Gln	Leu	Arg	Gly	Arg	Leu	Thr	Ser	Gln	Asp	155	160	165	
Trp	Glu	Arg	Val	His	Leu	Ile	Val	Ala	Gly	Gly	Tyr	Asp	Glu	Arg	170	175	180	
Val	Leu	Glu	Asn	Val	Glu	His	Tyr	Gln	Glu	Leu	Lys	Lys	Met	Val	185	190	195	
Gln	Gln	Ser	Asp	Leu	Gly	Gln	Tyr	Val	Thr	Phe	Leu	Arg	Ser	Phe	200	205	210	
Ser	Asp	Lys	Gln	Lys	Ile	Ser	Leu	Leu	His	Ser	Cys	Thr	Cys	Val	215	220	225	
Leu	Tyr	Thr	Pro	Ser	Asn	Glu	His	Phe	Gly	Ile	Val	Pro	Leu	Glu	230	235	240	
Ala	Met	Tyr	Met	Gln	Cys	Pro	Val	Ile	Ala	Val	Asn	Ser	Gly	Gly	245	250	255	
Pro	Leu	Glu	Ser	Ile	Asp	His	Ser	Val	Thr	Gly	Phe	Leu	Cys	Glu	260	265	270	

Pro Asp Pro Val His Phe Ser Glu Ala Ile Glu Lys Phe Ile Arg  
275 280 285

Glu Pro Ser Leu Lys Ala Thr Met Gly Leu Ala Gly Arg Ala Arg  
290 295 300

Val Lys Glu Lys Phe Ser Pro Glu Ala Phe Thr Glu Gln Leu Tyr  
305 310 315

Arg Tyr Val Thr Lys Leu Leu Val  
320

<210> 211  
<211> 1554  
<212> DNA  
<213> Homo sapiens

<400> 211  
gactacgccg atccgagacg tggctccctg ggcggcagaa ccatgttgga 50  
cttcgcgatc ttgcgcgtta ccttcttgct ggcgttggtg ggagccgtgc 100  
tctacctcta tccggcttcc agacaagctg caggaattcc agggattact 150  
ccaactgaag aaaaagatgg taatcttcca gatattgtga atagtggaag 200  
tttgcattgag ttcttggtta atttgcattg gagatatggg cctgtggtct 250  
ccttctggtt tggcaggcgc ctctgtggtta gtttgggcac tgttgatgta 300  
ctgaagcagc atatcaatcc caataagaca tcggaccctt ttgaaaccat 350  
gctgaagtca ttattaaggt atcaatctgg tgggtggcagt gtgagtgaag 400  
accacattgag gaaaaaattg tatgaaaatg gtgtgactga ttctctgaag 450  
agtaactttg ccctcctcct aaagctttca gaagaattat tagataaatg 500  
gctctcctac ccagagaccc agcacgtgcc cctcagccag catatgcttg 550  
gttttgctat gaagtctggt acacagattg taatgggtag tacatttgaa 600  
gatgatcagg aagtcattcg cttocagaag aatcatggca cagtttggtc 650  
tgagattgga aaaggctttc tagatgggtc acttgataaa aacatgactc 700  
ggaaaaaaca atatgaagat gccctcatgc aactggagtc tgttttaagg 750  
aacatcataa aagaacgaaa aggaaggaac ttcagtcaac atattttcat 800  
tgactcctta gtacaaggga accttaattg ccaacagatc ctagaagaca 850  
gtatgatatt ttctctggcc agttgcataa taactgcaaa attgtgtacc 900  
tgggcaatct gttttttaac cacctctgaa gaagttcaaa aaaaattata 950  
tgaagagata aaccaagttt ttggaaatgg tcctgttact ccagagaaaa 1000



	140		145		150
Asp Lys Trp Leu Ser Tyr Pro Glu Thr Gln His Val Pro Leu Ser	155		160		165
Gln His Met Leu Gly Phe Ala Met Lys Ser Val Thr Gln Met Val	170		175		180
Met Gly Ser Thr Phe Glu Asp Asp Gln Glu Val Ile Arg Phe Gln	185		190		195
Lys Asn His Gly Thr Val Trp Ser Glu Ile Gly Lys Gly Phe Leu	200		205		210
Asp Gly Ser Leu Asp Lys Asn Met Thr Arg Lys Lys Gln Tyr Glu	215		220		225
Asp Ala Leu Met Gln Leu Glu Ser Val Leu Arg Asn Ile Ile Lys	230		235		240
Glu Arg Lys Gly Arg Asn Phe Ser Gln His Ile Phe Ile Asp Ser	245		250		255
Leu Val Gln Gly Asn Leu Asn Asp Gln Gln Ile Leu Glu Asp Ser	260		265		270
Met Ile Phe Ser Leu Ala Ser Cys Ile Ile Thr Ala Lys Leu Cys	275		280		285
Thr Trp Ala Ile Cys Phe Leu Thr Thr Ser Glu Glu Val Gln Lys	290		295		300
Lys Leu Tyr Glu Glu Ile Asn Gln Val Phe Gly Asn Gly Pro Val	305		310		315
Thr Pro Glu Lys Ile Glu Gln Leu Arg Tyr Cys Gln His Val Leu	320		325		330
Cys Glu Thr Val Arg Thr Ala Lys Leu Thr Pro Val Ser Ala Gln	335		340		345
Leu Gln Asp Ile Glu Gly Lys Ile Asp Arg Phe Ile Ile Pro Arg	350		355		360
Glu Thr Leu Val Leu Tyr Ala Leu Gly Val Val Leu Gln Asp Pro	365		370		375
Asn Thr Trp Pro Ser Pro His Lys Phe Asp Pro Asp Arg Phe Asp	380		385		390
Asp Glu Leu Val Met Lys Thr Phe Ser Ser Leu Gly Phe Ser Gly	395		400		405
Thr Gln Glu Cys Pro Glu Leu Arg Phe Ala Tyr Met Val Thr Thr	410		415		420
Val Leu Leu Ser Val Leu Val Lys Arg Leu His Leu Leu Ser Val	425		430		435

Glu Gly Gln Val Ile Glu Thr Lys Tyr Glu Leu Val Thr Ser Ser  
 440 445 450

Arg Glu Glu Ala Trp Ile Thr Val Ser Lys Arg Tyr  
 455 460

<210> 213  
 <211> 759  
 <212> DNA  
 <213> Homo sapiens

<400> 213  
 ctagatttgt cggcttgccg ggagacttca ggagtcgctg tctctgaact 50  
 tccagcctca gagaccgccg cccttgctcc cgagggccat gggccgggtc 100  
 tcagggcttg tgccctctcg ctctctgacg ctctggcgc atctggtggt 150  
 cgtcatcacc ttattctggt cccgggacag caacatacag gcctgcctgc 200  
 ctctcacgtt ccccccgag gagtatgaca agcaggacat tcagctggtg 250  
 gccgcgctct ctgtcaccct gggcctcttt gcagtggagc tggccgggtt 300  
 cctctcagga gtctccatgt tcaacagcac ccagagcctc atctccattg 350  
 gggctcactg tagtgcatcc gtggccctgt ccttcttcat attcgagcgt 400  
 tgggagtgca ctacgtattg gtacatTTTT gtcttctgca gtgcccttcc 450  
 agctgtcact gaaatggctt tattcgtcac cgtctttggg ctgaaaaaga 500  
 aacccttctg attaccttca tgacgggaac ctaaggacga agcctacagg 550  
 ggcaagggcc gcttcgtatt cctggaagaa ggaaggcata ggcttcggtt 600  
 ttcccctcgg aaactgcttc tgctggagga tatgtgttg aataattacg 650  
 tcttgagtct gggattatcc gcattgtatt tagtgctttg taataaaata 700  
 tgttttgtag taacattaag acttatatac agtttttaggg gacaattaa 750  
 aaaaaaaaa 759

<210> 214  
 <211> 140  
 <212> PRT  
 <213> Homo sapiens

<400> 214  
 Met Gly Arg Val Ser Gly Leu Val Pro Ser Arg Phe Leu Thr Leu  
 1 5 10 15  
 Leu Ala His Leu Val Val Val Ile Thr Leu Phe Trp Ser Arg Asp  
 20 25 30  
 Ser Asn Ile Gln Ala Cys Leu Pro Leu Thr Phe Thr Pro Glu Glu  
 35 40 45

Tyr Asp Lys Gln Asp Ile Gln Leu Val Ala Ala Leu Ser Val Thr  
 50 55 60  
 Leu Gly Leu Phe Ala Val Glu Leu Ala Gly Phe Leu Ser Gly Val  
 65 70 75  
 Ser Met Phe Asn Ser Thr Gln Ser Leu Ile Ser Ile Gly Ala His  
 80 85 90  
 Cys Ser Ala Ser Val Ala Leu Ser Phe Phe Ile Phe Glu Arg Trp  
 95 100 105  
 Glu Cys Thr Thr Tyr Trp Tyr Ile Phe Val Phe Cys Ser Ala Leu  
 110 115 120  
 Pro Ala Val Thr Glu Met Ala Leu Phe Val Thr Val Phe Gly Leu  
 125 130 135  
 Lys Lys Lys Pro Phe  
 140

<210> 215  
 <211> 697  
 <212> DNA  
 <213> Homo sapiens

<400> 215  
 tcccgacc tgcgcctg ccactatgtc ccgcgctct atgctgcttg 50  
 cctgggctct cccagcctc ctgcgactcg gagcggctca ggagacagaa 100  
 gaccggcct gctgcagccc catagtgtccc cggaacgagt ggaaggccct 150  
 ggcatcagag tgcgcccagc acctgagcct gcccttacgc tatgtggtgg 200  
 tatcgcacac ggcgggcagc agctgcaaca ccccgccctc gtgccagcag 250  
 caggcccgga atgtgcagca ctaccacatg aagacactgg gctggtgcga 300  
 cgtgggctac aacttcctga ttggagaaga cgggctcgta tacgagggcc 350  
 gtggctggaa cttcacgggt gccactcag gtcacttatg gaaccccatg 400  
 tccattggca tcagcttcat gggcaactac atggatcggg tgccacacc 450  
 ccaggccatc cgggcagccc agggctctact ggctgcgggt gtggctcagg 500  
 gagccctgag gtccaactat gtgtcaaag gacaccggga tgtgcagcgt 550  
 aactctctc caggcaacca gctctaccac ctcatccaga attggccaca 600  
 ctaccgtcc cctgaggcc ctgtgatcc gcacccatt cctccctcc 650  
 catggccaaa aacccactg tctccttctc caataaagat gtagctc 697

<210> 216  
 <211> 196  
 <212> PRT

<213> Homo sapiens

<400> 216

Met Ser Arg Arg Ser Met Leu Leu Ala Trp Ala Leu Pro Ser Leu  
1 5 10 15  
Leu Arg Leu Gly Ala Ala Gln Glu Thr Glu Asp Pro Ala Cys Cys  
20 25 30  
Ser Pro Ile Val Pro Arg Asn Glu Trp Lys Ala Leu Ala Ser Glu  
35 40 45  
Cys Ala Gln His Leu Ser Leu Pro Leu Arg Tyr Val Val Val Ser  
50 55 60  
His Thr Ala Gly Ser Ser Cys Asn Thr Pro Ala Ser Cys Gln Gln  
65 70 75  
Gln Ala Arg Asn Val Gln His Tyr His Met Lys Thr Leu Gly Trp  
80 85 90  
Cys Asp Val Gly Tyr Asn Phe Leu Ile Gly Glu Asp Gly Leu Val  
95 100 105  
Tyr Glu Gly Arg Gly Trp Asn Phe Thr Gly Ala His Ser Gly His  
110 115 120  
Leu Trp Asn Pro Met Ser Ile Gly Ile Ser Phe Met Gly Asn Tyr  
125 130 135  
Met Asp Arg Val Pro Thr Pro Gln Ala Ile Arg Ala Ala Gln Gly  
140 145 150  
Leu Leu Ala Cys Gly Val Ala Gln Gly Ala Leu Arg Ser Asn Tyr  
155 160 165  
Val Leu Lys Gly His Arg Asp Val Gln Arg Thr Leu Ser Pro Gly  
170 175 180  
Asn Gln Leu Tyr His Leu Ile Gln Asn Trp Pro His Tyr Arg Ser  
185 190 195

Pro

<210> 217

<211> 1871

<212> DNA

<213> Homo sapiens

<400> 217

ctgggacccc gaaaagagaa ggggagagcg aggggacgag agcggaggag 50  
gaagatgcaa ctgactcgct gctgcttcgt gttcctggtg cagggtagcc 100  
tctatctggt catctgtggc caggatgatg gtcctcccgg ctacaggagac 150  
cctgagcgtg atgaccacga gggccagccc cggccccggg tgccctcgaa 200



gcggggccac atctcaccta agtcccgccc catggccaat tccactctcc 250  
tagggctgct ggccccgcct ggggaggctt ggggcattct tgggcagccc 300  
cccaaccgcc cgaaccacag cccccacccc tcagccaagg tgaagaaaat 350  
ctttggctgg ggcgacttct actccaacat caagacggtg gccctgaacc 400  
tgctcgtcac aggaagatt gtggaccatg gcaatgggac cttcagcgtc 450  
cacttccaac acaatgccac aggccaggga aacatctcca tcagcctcgt 500  
gccccccagt aaagctgtag agttccacca ggaacagcag atcttcatcg 550  
aagccaaggc ctccaaaatc ttcaactgcc ggatggagtg ggagaaggta 600  
gaacggggcc gcgggacctc gctttgcacc cacgaccag ccaagatctg 650  
ctcccagagac cacgctcaga gctcagccac ctggagctgc tcccagccct 700  
tcaaagtcgt ctgtgtctac atcgcttct acagcacgga ctatcggctg 750  
gtccagaagg tgtgccaga ttacaactac catagtata cccctacta 800  
cccatctggg tgaccggggg caggccacag aggccaggcc agggctggaa 850  
ggacaggcct gcccatgcag gagaccatct ggacaccggg cagggaaggg 900  
gttgggcctc aggcaggag gggggtggag acgaggagat gccaagtggg 950  
gccagggcca agtctcaagt ggcagagaaa ggggcccaag tgctggcccc 1000  
aacctgaagc tgtggagtga ctagatcaca ggagcactgg aggaggagtg 1050  
ggctctctgt gcagcctcac agggctttgc cacggagcca cagagagatg 1100  
ctgggtcccc gaggcctgtg ggcaggccga tcagtgtggc cccagatcaa 1150  
gtcatgggag gaagctaagc ccttggttct tgccatcctg aggaaagata 1200  
gcaacaggga gggggagatt tcatcagtgt ggacagcctg tcaacttagg 1250  
atggatggct gagagggtt cctaggagcc agtcagcagg gtgggtggg 1300  
gccagaggag ctctccagcc ctgcctagtg ggcgcctga gcccttgctc 1350  
gtgtgctgag catggcatga ggctgaagtg gcaaccctgg ggtctttgat 1400  
gtcttgacag attgaccatc tgtctccagc caggccaccc ctttccaaaa 1450  
ttccctcttc tgccagtact cccctgtac caccattgc tgatggcaca 1500  
cccatcctta agctaagaca ggacgattgt ggtcctccca cactaaggcc 1550  
acagcccata cgcgtgctgt gtgtccctct tccacccaa cccctgctgg 1600  
ctcctctggg agcatccatg tcccggagag gggtcctca acagtcagcc 1650

tcacctgtca gaccggggtt ctcccgatc tggatggcgc cggcctctca 1700  
gcagcgggca cgggtggggc ggggccgggc cgcagagcat gtgctggatc 1750  
tggtctgtgt gtctgtctgt ggggtggggg aggggagga agtcttgtga 1800  
aaccgctgat tgctgacttt tgtgtgaaga atcgtgttct tggagcagga 1850  
aataaagctt gccccggggc a 1871

<210> 218  
<211> 252  
<212> PRT  
<213> Homo sapiens

<400> 218  
Met Gln Leu Thr Arg Cys Cys Phe Val Phe Leu Val Gln Gly Ser  
1 5 10 15  
Leu Tyr Leu Val Ile Cys Gly Gln Asp Asp Gly Pro Pro Gly Ser  
20 25 30  
Glu Asp Pro Glu Arg Asp Asp His Glu Gly Gln Pro Arg Pro Arg  
35 40 45  
Val Pro Arg Lys Arg Gly His Ile Ser Pro Lys Ser Arg Pro Met  
50 55 60  
Ala Asn Ser Thr Leu Leu Gly Leu Leu Ala Pro Pro Gly Glu Ala  
65 70 75  
Trp Gly Ile Leu Gly Gln Pro Pro Asn Arg Pro Asn His Ser Pro  
80 85 90  
Pro Pro Ser Ala Lys Val Lys Lys Ile Phe Gly Trp Gly Asp Phe  
95 100 105  
Tyr Ser Asn Ile Lys Thr Val Ala Leu Asn Leu Leu Val Thr Gly  
110 115 120  
Lys Ile Val Asp His Gly Asn Gly Thr Phe Ser Val His Phe Gln  
125 130 135  
His Asn Ala Thr Gly Gln Gly Asn Ile Ser Ile Ser Leu Val Pro  
140 145 150  
Pro Ser Lys Ala Val Glu Phe His Gln Glu Gln Gln Ile Phe Ile  
155 160 165  
Glu Ala Lys Ala Ser Lys Ile Phe Asn Cys Arg Met Glu Trp Glu  
170 175 180  
Lys Val Glu Arg Gly Arg Arg Thr Ser Leu Cys Thr His Asp Pro  
185 190 195  
Ala Lys Ile Cys Ser Arg Asp His Ala Gln Ser Ser Ala Thr Trp  
200 205 210

Ser Cys Ser Gln Pro Phe Lys Val Val Cys Val Tyr Ile Ala Phe  
215 220 225

Tyr Ser Thr Asp Tyr Arg Leu Val Gln Lys Val Cys Pro Asp Tyr  
230 235 240

Asn Tyr His Ser Asp Thr Pro Tyr Tyr Pro Ser Gly  
245 250

<210> 219

<211> 2065

<212> DNA

<213> Homo sapiens

<400> 219

gtgaatgtga gggtttgatg actttcagat gtctaggaac cagagtgggt 50  
gcaggggccc caggcagggc tgattcttgg gggaggaga gtagggtaaa 100  
gggttctgca tgagctcctt aaaggacaaa ggtaacagag ccagcgagag 150  
agctcgaggg gagactttga cttcaagcca cagaattggg ggaagtgtgc 200  
gcgccgccgc cgccgtcgct cctgcagcgc tgtcgaccta gccgctagca 250  
tcttcccgag caccgggatc ccggggtagg aggcgacgcg ggcgagcacc 300  
agcgccagcc ggctgcggtt gccacacgg ctcaccatgg gctccgggcg 350  
ccgggcgctg tccgcggtgc cggccgtgct gctggtcctc acgctgccgg 400  
ggctgcccggt ctgggcacag aacgacacgg agcccatcgt gctggagggc 450  
aagtgtctgg tgggtgtgca ctcgaacccg gccacggact ccaagggctc 500  
ctcttcctcc ccgctgggga tatcggtccg ggcgccaac tccaaggtcg 550  
ccttctcggc ggtgcggagc accaaccacg agccatccga gatgagcaac 600  
aagacgcgca tcatttactt cgatcagatc ctggtgaatg tgggtaattt 650  
tttcacattg gagtctgtct ttgtagcacc aagaaaagga atttacagtt 700  
tcagttttca cgtgattaaa gtctaccaga gccaaactat ccaggttaac 750  
ttgatgttaa atggaaaacc agtaatatct gcctttgcgg gggacaaaga 800  
tgttactcgt gaagctgcc acaatgggtg cctgctctac ctagataaaag 850  
aggataaggt ttacctaaaa ctggagaaag gtaatttggt tggaggctgg 900  
cagtattcca cgttttctgg ctttctgggt ttccccctat aggattcaat 950  
ttctccatga tgttcatcca ggtgagggat gaccactcc tgagttattg 1000  
gaagatcatt ttttcatcat tggattgatg tcttttattg gtttctcatg 1050  
ggtggatatg gattctaagg attctagcct gtctgaacca atacaaaatt 1100



Gly Ile Ser Val Arg Ala Ala Asn Ser Lys Val Ala Phe Ser Ala  
65 70 75

Val Arg Ser Thr Asn His Glu Pro Ser Glu Met Ser Asn Lys Thr  
80 85 90

Arg Ile Ile Tyr Phe Asp Gln Ile Leu Val Asn Val Gly Asn Phe  
95 100 105

Phe Thr Leu Glu Ser Val Phe Val Ala Pro Arg Lys Gly Ile Tyr  
110 115 120

Ser Phe Ser Phe His Val Ile Lys Val Tyr Gln Ser Gln Thr Ile  
125 130 135

Gln Val Asn Leu Met Leu Asn Gly Lys Pro Val Ile Ser Ala Phe  
140 145 150

Ala Gly Asp Lys Asp Val Thr Arg Glu Ala Ala Thr Asn Gly Val  
155 160 165

Leu Leu Tyr Leu Asp Lys Glu Asp Lys Val Tyr Leu Lys Leu Glu  
170 175 180

Lys Gly Asn Leu Val Gly Gly Trp Gln Tyr Ser Thr Phe Ser Gly  
185 190 195

Phe Leu Val Phe Pro Leu  
200

<210> 221  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 221  
acggctcacc atgggctccg 20

<210> 222  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 222  
aggaagagga gcccttggag tccg 24

<210> 223  
<211> 40

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 223  
cgtgctggag ggcaagtgtc tgggtggtgtg cgactcgaac 40

<210> 224  
<211> 902  
<212> DNA  
<213> Homo sapiens

<400> 224  
cgggtggccat gactgoggcc gtgtttcttcg gctgcgcctt cattgccttc 50  
gggcctgcgc tcgcccttta tgtcttcacc atcgccatcg agccgttgcg 100  
tatcatcttc ctcacgcgcg gagctttctt ctggttggtg tctctactga 150  
tttcgtccct tgtttggttc atggcaagag tcattattga caacaaagat 200  
ggaccaacac agaaatatct gctgatcttt ggagcgtttg tctctgtcta 250  
tatccaagaa atgttccgat ttgcatatta taaactctta aaaaaagcca 300  
gtgaaggttt gaagagtata aaccaggtg agacagcacc ctctatgcga 350  
ctgctggcct atgtttctgg ctggggcttt ggaatcatga gtggagtatt 400  
ttcctttgtg aataccctat ctgactcctt ggggccaggc acagtgggca 450  
ttcatggaga ttctcctcaa ttcttccttt attcagcttt catgacgctg 500  
gtcattatct tgctgcatgt attctggggc attgtatttt ttgatggctg 550  
tgagaagaaa aagtggggca tcctccttat cgttctcctg acccacctgc 600  
tgggtgtcagc ccagaccttc ataagttctt attatggaat aaacctggcg 650  
tcagcattta taatcctggt gctcatgggc acctgggcat tottagctgc 700  
gggaggcagc tgccgaagcc tgaaactctg cctgctctgc caagacaaga 750  
actttctttt ttacaaccag cgctccagat aacctcaggg aaccagcact 800  
tcccaaaccg cagactacat ctttagagga agcacaactg tgcctttttc 850  
tgaaaatccc tttttctggt ggaattgaga aagaaataaa actatgcaga 900  
ta 902

<210> 225  
<211> 257  
<212> PRT

<213> Homo sapiens

<400> 225

Met Thr Ala Ala Val Phe Phe Gly Cys Ala Phe Ile Ala Phe Gly  
1 5 10 15  
Pro Ala Leu Ala Leu Tyr Val Phe Thr Ile Ala Ile Glu Pro Leu  
20 25 30  
Arg Ile Ile Phe Leu Ile Ala Gly Ala Phe Phe Trp Leu Val Ser  
35 40 45  
Leu Leu Ile Ser Ser Leu Val Trp Phe Met Ala Arg Val Ile Ile  
50 55 60  
Asp Asn Lys Asp Gly Pro Thr Gln Lys Tyr Leu Leu Ile Phe Gly  
65 70 75  
Ala Phe Val Ser Val Tyr Ile Gln Glu Met Phe Arg Phe Ala Tyr  
80 85 90  
Tyr Lys Leu Leu Lys Lys Ala Ser Glu Gly Leu Lys Ser Ile Asn  
95 100 105  
Pro Gly Glu Thr Ala Pro Ser Met Arg Leu Leu Ala Tyr Val Ser  
110 115 120  
Gly Leu Gly Phe Gly Ile Met Ser Gly Val Phe Ser Phe Val Asn  
125 130 135  
Thr Leu Ser Asp Ser Leu Gly Pro Gly Thr Val Gly Ile His Gly  
140 145 150  
Asp Ser Pro Gln Phe Phe Leu Tyr Ser Ala Phe Met Thr Leu Val  
155 160 165  
Ile Ile Leu Leu His Val Phe Trp Gly Ile Val Phe Phe Asp Gly  
170 175 180  
Cys Glu Lys Lys Lys Trp Gly Ile Leu Leu Ile Val Leu Leu Thr  
185 190 195  
His Leu Leu Val Ser Ala Gln Thr Phe Ile Ser Ser Tyr Tyr Gly  
200 205 210  
Ile Asn Leu Ala Ser Ala Phe Ile Ile Leu Val Leu Met Gly Thr  
215 220 225  
Trp Ala Phe Leu Ala Ala Gly Gly Ser Cys Arg Ser Leu Lys Leu  
230 235 240  
Cys Leu Leu Cys Gln Asp Lys Asn Phe Leu Leu Tyr Asn Gln Arg  
245 250 255  
Ser Arg

<210> 226

<211> 3939  
<212> DNA  
<213> Homo sapiens

<400> 226  
cggcaaccag ccgccgccac caccgctgcc actgccgcc tgcgggggcc 50  
atgttcgctc tgggcttgcc cttcttggtg ctcttggtgg octcggtoga 100  
gagccatctg ggggttcttg ggccaagaa cgtctcgcag aaagacgccg 150  
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<211> 832

<212> PRT

<213> Homo sapiens

<400> 227

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Lys	Asp	Ala	Glu	Phe	Glu	Arg	Thr	Tyr	Val	Asp	Glu	Val	Asn	Ser		35	40	45
Glu	Leu	Val	Asn	Ile	Tyr	Thr	Phe	Asn	His	Thr	Val	Thr	Arg	Asn		50	55	60
Arg	Thr	Glu	Gly	Val	Arg	Val	Ser	Val	Asn	Val	Leu	Asn	Lys	Gln		65	70	75
Lys	Gly	Ala	Pro	Leu	Leu	Phe	Val	Val	Arg	Gln	Lys	Glu	Ala	Val		80	85	90
Val	Ser	Phe	Gln	Val	Pro	Leu	Ile	Leu	Arg	Gly	Met	Phe	Gln	Arg		95	100	105
Lys	Tyr	Leu	Tyr	Gln	Lys	Val	Glu	Arg	Thr	Leu	Cys	Gln	Pro	Pro		110	115	120
Thr	Lys	Asn	Glu	Ser	Glu	Ile	Gln	Phe	Phe	Tyr	Val	Asp	Val	Ser		125	130	135
Thr	Leu	Ser	Pro	Val	Asn	Thr	Thr	Tyr	Gln	Leu	Arg	Val	Ser	Arg		140	145	150
Met	Asp	Asp	Phe	Val	Leu	Arg	Thr	Gly	Glu	Gln	Phe	Ser	Phe	Asn		155	160	165
Thr	Thr	Ala	Ala	Gln	Pro	Gln	Tyr	Phe	Lys	Tyr	Glu	Phe	Pro	Glu		170	175	180
Gly	Val	Asp	Ser	Val	Ile	Val	Lys	Val	Thr	Ser	Asn	Lys	Ala	Phe		185	190	195
Pro	Cys	Ser	Val	Ile	Ser	Ile	Gln	Asp	Val	Leu	Cys	Pro	Val	Tyr		200	205	210
Asp	Leu	Asp	Asn	Asn	Val	Ala	Phe	Ile	Gly	Met	Tyr	Gln	Thr	Met		215	220	225
Thr	Lys	Lys	Ala	Ala	Ile	Thr	Val	Gln	Arg	Lys	Asp	Phe	Pro	Ser		230	235	240
Asn	Ser	Phe	Tyr	Val	Val	Val	Val	Val	Lys	Thr	Glu	Asp	Gln	Ala		245	250	255
Cys	Gly	Gly	Ser	Leu	Pro	Phe	Tyr	Pro	Phe	Ala	Glu	Asp	Glu	Pro		260	265	270
Val	Asp	Gln	Gly	His	Arg	Gln	Lys	Thr	Leu	Ser	Val	Leu	Val	Ser		275	280	285
Gln	Ala	Val	Thr	Ser	Glu	Ala	Tyr	Val	Ser	Gly	Met	Leu	Phe	Cys		290	295	300
Leu	Gly	Ile	Phe	Leu	Ser	Phe	Tyr	Leu	Leu	Thr	Val	Leu	Leu	Ala		305	310	315
Cys	Trp	Glu	Asn	Trp	Arg	Gln	Lys	Lys	Lys	Thr	Leu	Leu	Val	Ala				

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Ile Asp Arg Ala Cys Pro Glu Ser Gly His Pro Arg Val Leu Ala	335		340		345
Asp Ser Phe Pro Gly Ser Ser Pro Tyr Glu Gly Tyr Asn Tyr Gly	350		355		360
Ser Phe Glu Asn Val Ser Gly Ser Thr Asp Gly Leu Val Asp Ser	365		370		375
Ala Gly Thr Gly Asp Leu Ser Tyr Gly Tyr Gln Gly Arg Ser Phe	380		385		390
Glu Pro Val Gly Thr Arg Pro Arg Val Asp Ser Met Ser Ser Val	395		400		405
Glu Glu Asp Asp Tyr Asp Thr Leu Thr Asp Ile Asp Ser Asp Lys	410		415		420
Asn Val Ile Arg Thr Lys Gln Tyr Leu Tyr Val Ala Asp Leu Ala	425		430		435
Arg Lys Asp Lys Arg Val Leu Arg Lys Lys Tyr Gln Ile Tyr Phe	440		445		450
Trp Asn Ile Ala Thr Ile Ala Val Phe Tyr Ala Leu Pro Val Val	455		460		465
Gln Leu Val Ile Thr Tyr Gln Thr Val Val Asn Val Thr Gly Asn	470		475		480
Gln Asp Ile Cys Tyr Tyr Asn Phe Leu Cys Ala His Pro Leu Gly	485		490		495
Asn Leu Ser Ala Phe Asn Asn Ile Leu Ser Asn Leu Gly Tyr Ile	500		505		510
Leu Leu Gly Leu Leu Phe Leu Leu Ile Ile Leu Gln Arg Glu Ile	515		520		525
Asn His Asn Arg Ala Leu Leu Arg Asn Asp Leu Cys Ala Leu Glu	530		535		540
Cys Gly Ile Pro Lys His Phe Gly Leu Phe Tyr Ala Met Gly Thr	545		550		555
Ala Leu Met Met Glu Gly Leu Leu Ser Ala Cys Tyr His Val Cys	560		565		570
Pro Asn Tyr Thr Asn Phe Gln Phe Asp Thr Ser Phe Met Tyr Met	575		580		585
Ile Ala Gly Leu Cys Met Leu Lys Leu Tyr Gln Lys Arg His Pro	590		595		600
Asp Ile Asn Ala Ser Ala Tyr Ser Ala Tyr Ala Cys Leu Ala Ile	605		610		615

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Asp	Ser	Gly	Ile	Phe	Arg	Arg	Ile	Leu	His	Val	Leu	Tyr	Thr	Asp	
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Cys	Ile	Arg	Gln	Cys	Ser	Gly	Pro	Leu	Tyr	Val	Asp	Arg	Met	Val	
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Leu	Leu	Val	Met	Gly	Asn	Val	Ile	Asn	Trp	Ser	Leu	Ala	Ala	Tyr	
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Gly	Leu	Ile	Met	Arg	Pro	Asn	Asp	Phe	Ala	Ser	Tyr	Leu	Leu	Ala	
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Ile	Gly	Ile	Cys	Asn	Leu	Leu	Leu	Tyr	Phe	Ala	Phe	Tyr	Ile	Ile	
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Met	Lys	Leu	Arg	Ser	Gly	Glu	Arg	Ile	Lys	Leu	Ile	Pro	Leu	Leu	
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Cys	Ile	Val	Cys	Thr	Ser	Val	Val	Trp	Gly	Phe	Ala	Leu	Phe	Phe	
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Phe	Phe	Gln	Gly	Leu	Ser	Thr	Trp	Gln	Lys	Thr	Pro	Ala	Glu	Ser	
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Arg	Glu	His	Asn	Arg	Asp	Cys	Ile	Leu	Leu	Asp	Phe	Phe	Asp	Asp	
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His	Asp	Ile	Trp	His	Phe	Leu	Ser	Ser	Ile	Ala	Met	Phe	Gly	Ser	
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<211> 2848

<212> DNA

<213> Homo sapiens

<400> 228

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<400> 229  
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Leu Pro Arg Glu	Gly Ala Glu Gly Gln Ile	Val Leu Ser Gly Asp			
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Ser Gly Lys Ala	Thr Glu Gly Pro Phe Ala	Met Asp Pro Asp Ser			
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Gly Phe Leu Leu	Val Thr Arg Ala Leu Asp	Arg Glu Glu Gln Ala			
	80		85		90
Glu Tyr Gln Leu	Gln Val Thr Leu Glu Met	Gln Asp Gly His Val			
	95		100		105
Leu Trp Gly Pro	Gln Pro Val Leu Val His	Val Lys Asp Glu Asn			
	110		115		120
Asp Gln Val Pro	His Phe Ser Gln Ala Ile	Tyr Arg Ala Arg Leu			
	125		130		135
Ser Arg Gly Thr	Arg Pro Gly Ile Pro Phe	Leu Phe Leu Glu Ala			
	140		145		150
Ser Asp Arg Asp	Glu Pro Gly Thr Ala Asn	Ser Asp Leu Arg Phe			
	155		160		165
His Ile Leu Ser	Gln Ala Pro Ala Gln Pro	Ser Pro Asp Met Phe			
	170		175		180
Gln Leu Glu Pro	Arg Leu Gly Ala Leu Ala	Leu Ser Pro Lys Gly			
	185		190		195
Ser Thr Ser Leu	Asp His Ala Leu Glu Arg	Thr Tyr Gln Leu Leu			
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Val Gln Val Lys	Asp Met Gly Asp Gln Ala	Ser Gly His Gln Ala			
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Thr Ala Thr Val	Glu Val Ser Ile Ile Glu	Ser Thr Trp Val Ser			
	230		235		240
Leu Glu Pro Ile	His Leu Ala Glu Asn Leu	Lys Val Leu Tyr Pro			
	245		250		255
His His Met Ala	Gln Val His Trp Ser Gly	Gly Asp Val His Tyr			
	260		265		270
His Leu Glu Ser	His Pro Pro Gly Pro Phe	Glu Val Asn Ala Glu			
	275		280		285
Gly Asn Leu Tyr	Val Thr Arg Glu Leu Asp	Arg Glu Ala Gln Ala			
	290		295		300
Glu Tyr Leu Leu	Gln Val Arg Ala Gln Asn	Ser His Gly Glu Asp			
	305		310		315



Tyr Ala Ala Pro	Leu Glu Leu His Val	Leu Val Met Asp Glu Asn	320	325	330
Asp Asn Val Pro	Ile Cys Pro Pro Arg	Asp Pro Thr Val Ser Ile	335	340	345
Pro Glu Leu Ser	Pro Pro Gly Thr Glu	Val Thr Arg Leu Ser Ala	350	355	360
Glu Asp Ala Asp	Ala Pro Gly Ser Pro	Asn Ser His Val Val Tyr	365	370	375
Gln Leu Leu Ser	Pro Glu Pro Glu Asp	Gly Val Glu Gly Arg Ala	380	385	390
Phe Gln Val Asp	Pro Thr Ser Gly Ser	Val Thr Leu Gly Val Leu	395	400	405
Pro Leu Arg Ala	Gly Gln Asn Ile Leu	Leu Leu Val Leu Ala Met	410	415	420
Asp Leu Ala Gly	Ala Glu Gly Gly Phe	Ser Ser Thr Cys Glu Val	425	430	435
Glu Val Ala Val	Thr Asp Ile Asn Asp	His Ala Pro Glu Phe Ile	440	445	450
Thr Ser Gln Ile	Gly Pro Ile Ser Leu	Pro Glu Asp Val Glu Pro	455	460	465
Gly Thr Leu Val	Ala Met Leu Thr Ala	Ile Asp Ala Asp Leu Glu	470	475	480
Pro Ala Phe Arg	Leu Met Asp Phe Ala	Ile Glu Arg Gly Asp Thr	485	490	495
Glu Gly Thr Phe	Gly Leu Asp Trp Glu	Pro Asp Ser Gly His Val	500	505	510
Arg Leu Arg Leu	Cys Lys Asn Leu Ser	Tyr Glu Ala Ala Pro Ser	515	520	525
His Glu Val Val	Val Val Val Gln Ser	Val Ala Lys Leu Val Gly	530	535	540
Pro Gly Pro Gly	Pro Gly Ala Thr Ala	Thr Val Thr Val Leu Val	545	550	555
Glu Arg Val Met	Pro Pro Pro Lys Leu	Asp Gln Glu Ser Tyr Glu	560	565	570
Ala Ser Val Pro	Ile Ser Ala Pro Ala	Gly Ser Phe Leu Leu Thr	575	580	585
Ile Gln Pro Ser	Asp Pro Ile Ser Arg	Thr Leu Arg Phe Ser Leu	590	595	600
Val Asn Asp Ser	Glu Gly Trp Leu Cys	Ile Glu Lys Phe Ser Gly			

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Glu Val His Thr	Ala Gln Ser Leu Gln	Gly Ala Gln Pro Gly	Asp		
	620	625	630		
Thr Tyr Thr Val	Leu Val Glu Ala Gln	Asp Thr Ala Leu Thr	Leu		
	635	640	645		
Ala Pro Val Pro	Ser Gln Tyr Leu Cys	Thr Pro Arg Gln Asp	His		
	650	655	660		
Gly Leu Ile Val	Ser Gly Pro Ser Lys	Asp Pro Asp Leu Ala	Ser		
	665	670	675		
Gly His Gly Pro	Tyr Ser Phe Thr Leu	Gly Pro Asn Pro Thr	Val		
	680	685	690		
Gln Arg Asp Trp	Arg Leu Gln Thr Leu	Asn Gly Ser His Ala	Tyr		
	695	700	705		
Leu Thr Leu Ala	Leu His Trp Val Glu	Pro Arg Glu His Ile	Ile		
	710	715	720		
Pro Val Val Val	Ser His Asn Ala Gln	Met Trp Gln Leu Leu	Val		
	725	730	735		
Arg Val Ile Val	Cys Arg Cys Asn Val	Glu Gly Gln Cys Met	Arg		
	740	745	750		
Lys Val Gly Arg	Met Lys Gly Met Pro	Thr Lys Leu Ser Ala	Val		
	755	760	765		
Gly Ile Leu Val	Gly Thr Leu Val Ala	Ile Gly Ile Phe Leu	Ile		
	770	775	780		
Leu Ile Phe Thr	His Trp Thr Met Ser	Arg Lys Lys Asp Pro	Asp		
	785	790	795		
Gln Pro Ala Asp	Ser Val Pro Leu Lys	Ala Thr Val			
	800	805			

<210> 230  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-50  
 <223> Synthetic construct.

<400> 230  
 cgccttaccg cgcagccccga agattcacta tgggtgaaaat cgccttcaat 50

<210> 231  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequeunce

<220>  
 <221> Artificial Sequence  
 <222> full  
 <223> Synthetic oligonucleotide probe

<400> 231  
 cctgagctgt aaccccactc cagg 24

<210> 232  
 <211> 23  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 232  
 agagtctgtc ccagctatct tgt 23

<210> 233  
 <211> 2786  
 <212> DNA  
 <213> Homo sapiens

<400> 233  
 ccgggggacat gaggtggata ctgttcattg gggcccttat tgggtccagc 50  
 atctgtggcc aagaaaaatt ttttggggac caagtattga ggattaatgt 100  
 cagaaatgga gacgagatca gcaaattgag tcaactagtg aattcaaaca 150  
 acttgaagct caatttctgg aaatctccct cctccttcaa tcggcctgtg 200  
 gatgtcctgg tcccatctgt cagtctgcag gcatttaaact ccttctgag 250  
 atcccagggc ttagagtacg cagtgacaat tgaggacctg caggcccttt 300  
 tagacaatga agatgatgaa atgcaacaca atgaaggga agaacggagc 350  
 agtaataact tcaactacgg ggcttaccat tccctggaag ctatttacca 400  
 cgagatggac aacattgccg cagactttcc tgacctggcg aggagggtga 450  
 agattggaca ttogtttgaa aaccggccga tgtatgtact gaagttcagc 500  
 actgggaaag gcgtgaggcg gccggccgtt tggctgaatg caggcatcca 550  
 ttcccagagag tggatctccc aggccactgc aatctggacg gcaaggaaga 600  
 ttgtatctga ttaccagagg gatccagcta tcacctccat cttggagaaa 650  
 atggatatatt tcttgttgcc tgtggccaat cctgatggat atgtgtatac 700  
 tcaaactcaa aaccgattat ggaggaagac gcggtcccga aatcctggaa 750  
 gctcctgcat tgggtgtgac ccaaatagaa actggaacgc tagttttgca 800  
 ggaaagggag ccagcgacaa cccttgctcc gaagtgtacc atggaccca 850



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 cctoctcttt gccttttgaa ctacttcaa agatctaggc ctcatcttac 2400  
 aggtcctaaa tcactcatct ggcctggata atctcactgc cctggcacat 2450  
 toccatttgt gctgtgggtg atcctgtgtt tccttgtcct ggtttgtgtg 2500  
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 tgttgttgtt ttgtttttgt ttttttgctt ttaccaaaca tgtctgtaaa 2700  
 tcttaacctc ctgcctagga tttgtacagc atctggtgtg tgcttataag 2750  
 ccaataaata ttcaatgtga aaaaaaaaaa aaaaaa 2786

<210> 234

<211> 421

<212> PRT

<213> Homo sapiens

<400> 234

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Cys	Gly	Gln	Glu	Lys	Phe	Phe	Gly	Asp	Gln	Val	Leu	Arg	Ile	Asn
				20					25					30
Val	Arg	Asn	Gly	Asp	Glu	Ile	Ser	Lys	Leu	Ser	Gln	Leu	Val	Asn
				35					40					45
Ser	Asn	Asn	Leu	Lys	Leu	Asn	Phe	Trp	Lys	Ser	Pro	Ser	Ser	Phe
				50					55					60
Asn	Arg	Pro	Val	Asp	Val	Leu	Val	Pro	Ser	Val	Ser	Leu	Gln	Ala
				65					70					75
Phe	Lys	Ser	Phe	Leu	Arg	Ser	Gln	Gly	Leu	Glu	Tyr	Ala	Val	Thr
				80					85					90
Ile	Glu	Asp	Leu	Gln	Ala	Leu	Leu	Asp	Asn	Glu	Asp	Asp	Glu	Met
				95					100					105
Gln	His	Asn	Glu	Gly	Gln	Glu	Arg	Ser	Ser	Asn	Asn	Phe	Asn	Tyr
				110					115					120
Gly	Ala	Tyr	His	Ser	Leu	Glu	Ala	Ile	Tyr	His	Glu	Met	Asp	Asn
				125					130					135
Ile	Ala	Ala	Asp	Phe	Pro	Asp	Leu	Ala	Arg	Arg	Val	Lys	Ile	Gly
				140					145					150
His	Ser	Phe	Glu	Asn	Arg	Pro	Met	Tyr	Val	Leu	Lys	Phe	Ser	Thr
				155					160					165

Gly	Lys	Gly	Val	Arg	Arg	Pro	Ala	Val	Trp	Leu	Asn	Ala	Gly	Ile	170	175	180
His	Ser	Arg	Glu	Trp	Ile	Ser	Gln	Ala	Thr	Ala	Ile	Trp	Thr	Ala	185	190	195
Arg	Lys	Ile	Val	Ser	Asp	Tyr	Gln	Arg	Asp	Pro	Ala	Ile	Thr	Ser	200	205	210
Ile	Leu	Glu	Lys	Met	Asp	Ile	Phe	Leu	Leu	Pro	Val	Ala	Asn	Pro	215	220	225
Asp	Gly	Tyr	Val	Tyr	Thr	Gln	Thr	Gln	Asn	Arg	Leu	Trp	Arg	Lys	230	235	240
Thr	Arg	Ser	Arg	Asn	Pro	Gly	Ser	Ser	Cys	Ile	Gly	Ala	Asp	Pro	245	250	255
Asn	Arg	Asn	Trp	Asn	Ala	Ser	Phe	Ala	Gly	Lys	Gly	Ala	Ser	Asp	260	265	270
Asn	Pro	Cys	Ser	Glu	Val	Tyr	His	Gly	Pro	His	Ala	Asn	Ser	Glu	275	280	285
Val	Glu	Val	Lys	Ser	Val	Val	Asp	Phe	Ile	Gln	Lys	His	Gly	Asn	290	295	300
Phe	Lys	Gly	Phe	Ile	Asp	Leu	His	Ser	Tyr	Ser	Gln	Leu	Leu	Met	305	310	315
Tyr	Pro	Tyr	Gly	Tyr	Ser	Val	Lys	Lys	Ala	Pro	Asp	Ala	Glu	Glu	320	325	330
Leu	Asp	Lys	Val	Ala	Arg	Leu	Ala	Ala	Lys	Ala	Leu	Ala	Ser	Val	335	340	345
Ser	Gly	Thr	Glu	Tyr	Gln	Val	Gly	Pro	Thr	Cys	Thr	Thr	Val	Tyr	350	355	360
Pro	Ala	Ser	Gly	Ser	Ser	Ile	Asp	Trp	Ala	Tyr	Asp	Asn	Gly	Ile	365	370	375
Lys	Phe	Ala	Phe	Thr	Phe	Glu	Leu	Arg	Asp	Thr	Gly	Thr	Tyr	Gly	380	385	390
Phe	Leu	Leu	Pro	Ala	Asn	Gln	Ile	Ile	Pro	Thr	Ala	Glu	Glu	Thr	395	400	405
Trp	Leu	Gly	Leu	Lys	Thr	Ile	Met	Glu	His	Val	Arg	Asp	Asn	Leu	410	415	420

Tyr

<210> 235  
 <211> 1743  
 <212> DNA  
 <213> Homo sapiens

<400> 235

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 tgttccaaaa tggcatctta cttttatgga gtactctttg ctgttggcct 100  
 ctgtgctcca atctactgtg tgtccccggc caatgcccc agtgcatacc 150  
 cccgcccttc ctccacaaag agcaccctg cctcacaggt gtattccctc 200  
 aacaccgact ttgccttccg cctataccgc aggctggttt tggagacccc 250  
 gagtcagaac atcttcttct cccctgtgag tgtctccact tccctggcca 300  
 tgctctccct tggggcccac tcagtcacca agaccagat tctccagggc 350  
 ctgggcttca acctcacaca cacaccagag tctgccatcc accagggctt 400  
 ccagcaoctg gttcactcac tgactgttcc cagcaaagac ctgacctga 450  
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 gggagatgcc gtggccttct ttgtcctccc tagcaagggc aagatgaggc 900  
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 ctctacaat ctggaaacca tcctcccgaa gatgggcac caaatgcct 1050  
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 gtttctaaag caaccacaa ggctgtgctg gatgtcagtg aagagggcac 1150  
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 gtccctctta cttcactgtc tccttcaata ggaccttct gatgatgatt 1250  
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 cactaaatcc taggtgggaa atggcctgtt aactgatggc acattgctaa 1350  
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aatcaccaaa ccatcaacag ggaccccagt cacaagccaa caccattaa 1500  
 cccagtcag tgcccttttc cacaattct cccaggtaac tagcttcag 1550  
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<210> 236  
 <211> 417  
 <212> PRT  
 <213> Homo sapiens

<400> 236  
 Met Ala Ser Tyr Leu Tyr Gly Val Leu Phe Ala Val Gly Leu Cys  
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 Ala Pro Ile Tyr Cys Val Ser Pro Ala Asn Ala Pro Ser Ala Tyr  
 20 25 30  
 Pro Arg Pro Ser Ser Thr Lys Ser Thr Pro Ala Ser Gln Val Tyr  
 35 40 45  
 Ser Leu Asn Thr Asp Phe Ala Phe Arg Leu Tyr Arg Arg Leu Val  
 50 55 60  
 Leu Glu Thr Pro Ser Gln Asn Ile Phe Phe Ser Pro Val Ser Val  
 65 70 75  
 Ser Thr Ser Leu Ala Met Leu Ser Leu Gly Ala His Ser Val Thr  
 80 85 90  
 Lys Thr Gln Ile Leu Gln Gly Leu Gly Phe Asn Leu Thr His Thr  
 95 100 105  
 Pro Glu Ser Ala Ile His Gln Gly Phe Gln His Leu Val His Ser  
 110 115 120  
 Leu Thr Val Pro Ser Lys Asp Leu Thr Leu Lys Met Gly Ser Ala  
 125 130 135  
 Leu Phe Val Lys Lys Glu Leu Gln Leu Gln Ala Asn Phe Leu Gly  
 140 145 150  
 Asn Val Lys Arg Leu Tyr Glu Ala Glu Val Phe Ser Thr Asp Phe  
 155 160 165  
 Ser Asn Pro Ser Ile Ala Gln Ala Arg Ile Asn Ser His Val Lys  
 170 175 180  
 Lys Lys Thr Gln Gly Lys Val Val Asp Ile Ile Gln Gly Leu Asp  
 185 190 195  
 Leu Leu Thr Ala Met Val Leu Val Asn His Ile Phe Phe Lys Ala



200	205	210
Lys Trp Glu Lys Pro Phe His Leu Glu	Tyr Thr Arg Lys Asn Phe	
215	220	225
Pro Phe Leu Val Gly Glu Gln Val Thr	Val Gln Val Pro Met Met	
230	235	240
His Gln Lys Glu Gln Phe Ala Phe Gly	Val Asp Thr Glu Leu Asn	
245	250	255
Cys Phe Val Leu Gln Met Asp Tyr Lys	Gly Asp Ala Val Ala Phe	
260	265	270
Phe Val Leu Pro Ser Lys Gly Lys Met	Arg Gln Leu Glu Gln Ala	
275	280	285
Leu Ser Ala Arg Thr Leu Ile Lys Trp	Ser His Ser Leu Gln Lys	
290	295	300
Arg Trp Ile Glu Val Phe Ile Pro Arg	Phe Ser Ile Ser Ala Ser	
305	310	315
Tyr Asn Leu Glu Thr Ile Leu Pro Lys	Met Gly Ile Gln Asn Ala	
320	325	330
Phe Asp Lys Asn Ala Asp Phe Ser Gly	Ile Ala Lys Arg Asp Ser	
335	340	345
Leu Gln Val Ser Lys Ala Thr His Lys	Ala Val Leu Asp Val Ser	
350	355	360
Glu Glu Gly Thr Glu Ala Thr Ala Ala	Thr Thr Thr Lys Phe Ile	
365	370	375
Val Arg Ser Lys Asp Gly Pro Ser Tyr	Phe Thr Val Ser Phe Asn	
380	385	390
Arg Thr Phe Leu Met Met Ile Thr Asn	Lys Ala Thr Asp Gly Ile	
395	400	405
Leu Phe Leu Gly Lys Val Glu Asn Pro	Thr Lys Ser	
410	415	

<210> 237

<211> 23

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 237

caaccatgca aggacagggc agg 23

<210> 238

<211> 47  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-47  
 <223> Synthetic construct.

<400> 238  
 ctttgctgtt ggcctctgtg ctcccaacca tgcaaggaca gggcagg 47

<210> 239  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 239  
 tgactcgggg tctccaaaac cagc 24

<210> 240  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 240  
 ggtataggcg gaaggcaaag tcgg 24

<210> 241  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 241  
 ggcatcttac ctttatggag tactctttgc tgttgccctc tgtgctcc 48

<210> 242  
 <211> 2436  
 <212> DNA  
 <213> Homo sapiens

<400> 242  
 ggctgaccgt gctacattgc ctggaggaag cctaaggaac ccaggcatcc 50

agctgcccac gcctgagtc aagattcttc ccaggaacac aaacgtagga 100  
 gaccacgct cctggaagca ccagccttta tctcttcacc ttcaagtccc 150  
 ctttctcaag aatcctctgt tctttgccct cttaaagtctt ggtacatcta 200  
 ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgcag 250  
 aaaggaaatg ttctccttat gtttgggtcta ctattgcatt tagaagctgc 300  
 aacaaattcc aatgagacta gcacctctgc caaacttgga tccagtgtga 350  
 tctccagtgg agccagcaca gccaccaact ctgggtccag tgtgacctcc 400  
 agtgggggtca gcacagccac catctcaggg tccagcgtga cctccaatgg 450  
 ggtcagcata gtcaccaact ctgagttcca tacaacctcc agtgggatca 500  
 gcacagccac caactctgag ttcagcacag cgtccagtgg gatcagcata 550  
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 caactctgag tccagcacac cctccagtgg ggccagcaca gtcaccaact 650  
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 ctgagtccag cagcacctcc agtggggcca gcacagccac caactctgag 1150  
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 cacaacctcc agtggggccg gcacagccac caactctgag tccagcacag 1250  
 tgtccagtgg gatcagcaca gtcaccaatt ctgagtccag cacacctcc 1300  
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 ggccaacaca gccaccaact ctgagtccag cacagtgtcc agtggggcca 1400  
 gcaactgccac caactctgag tccagcaca cctccagtgg ggtcagcaca 1450  
 gccaccaact ctgagtccag cacaacctcc agtggggcta gcacagccac 1500



Thr	Asn	Ser	Glu	Phe	His	Thr	Thr	Ser	Ser	Gly	Ile	Ser	Thr	Ala	
				80					85					90	
Thr	Asn	Ser	Glu	Phe	Ser	Thr	Ala	Ser	Ser	Gly	Ile	Ser	Ile	Ala	
				95					100					105	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				110					115					120	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Ser	Thr	Val	
				125					130					135	
Thr	Asn	Ser	Gly	Ser	Ser	Val	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				140					145					150	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				155					160					165	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Leu	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				170					175					180	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				185					190					195	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				200					205					210	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Arg	Ala	Ser	Thr	Ala	
				215					220					225	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				230					235					240	
Thr	Asn	Ser	Glu	Ser	Arg	Thr	Thr	Ser	Asn	Gly	Ala	Gly	Thr	Ala	
				245					250					255	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				260					265					270	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				275					280					285	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				290					295					300	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Ser	Thr	Ala	
				305					310					315	
Thr	Asn	Ser	Asp	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Gly	Thr	Ala	
				320					325					330	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Val	Ser	Ser	Gly	Ile	Ser	Thr	Val	
				335					340					345	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Pro	Ser	Ser	Gly	Ala	Asn	Thr	Ala	
				350					355					360	
Thr	Asn	Ser	Glu	Ser	Ser	Thr	Thr	Ser	Ser	Gly	Ala	Asn	Thr	Ala	

	365		370		375
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ala Ser Thr Ala	380		385		390
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Val Ser Thr Ala	395		400		405
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Ser Thr Ala	410		415		420
Thr Asn Ser Asp Ser Ser Thr Thr Ser Ser Glu Ala Ser Thr Ala	425		430		435
Thr Asn Ser Glu Ser Ser Thr Val Ser Ser Gly Ile Ser Thr Val	440		445		450
Thr Asn Ser Glu Ser Ser Thr Thr Ser Ser Gly Ala Asn Thr Ala	455		460		465
Thr Asn Ser Gly Ser Ser Val Thr Ser Ala Gly Ser Gly Thr Ala	470		475		480
Ala Leu Thr Gly Met His Thr Thr Ser His Ser Ala Ser Thr Ala	485		490		495
Val Ser Glu Ala Lys Pro Gly Gly Ser Leu Val Pro Trp Glu Ile	500		505		510
Phe Leu Ile Thr Leu Val Ser Val Val Ala Ala Val Gly Leu Phe	515		520		525
Ala Gly Leu Phe Phe Cys Val Arg Asn Ser Leu Ser Leu Arg Asn	530		535		540
Thr Phe Asn Thr Ala Val Tyr His Pro His Gly Leu Asn His Gly	545		550		555
Leu Gly Pro Gly Pro Gly Gly Asn His Gly Ala Pro His Arg Pro	560		565		570
Arg Trp Ser Pro Asn Trp Phe Trp Arg Arg Pro Val Ser Ser Ile	575		580		585
Ala Met Glu Met Ser Gly Arg Asn Ser Gly Pro	590		595		

<210> 244

<211> 26

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-26

<223> Synthetic construct.

<400> 244

gaagcaccag cctttatctc ttcacc 26

<210> 245

<211> 24

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-24

<223> Synthetic sequence.

<400> 245

gtcagagttg gtggctgtgc tagc 24

<210> 246

<211> 48

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-48

<223> Synthetic construct.

<400> 246

ggaccaggc atcttgcttt ccagccacaa agagacagat gaagatgc 48

<210> 247

<211> 957

<212> DNA

<213> Homo sapiens

<400> 247

gggagagagg ataaatagca gcgtggcttc cctggctcct ctctgcatcc 50

ttcccgacct tcccagcaat atgcatcttg cacgtctggt cggtcctgc 100

tccctccttc tgctactggg ggccctgtct ggatgggcgg ccagcgatga 150

ccccattgag aaggtcattg aagggatcaa ccgagggctg agcaatgcag 200

agagagaggt gggcaaggcc ctggatggca tcaacagtgg aatcacgcat 250

gccggaaggg aagtggagaa ggttttcaac ggacttagca acatggggag 300

ccacaccggc aaggagttgg acaaaggcgt ccaggggctc aaccacggca 350

tggacaaggt tgcccatgag atcaaccatg gtattggaca agcaggaaag 400

gaagcagaga agcttggcca tgggggtcaac aacgctgctg gacaggccgg 450

gaaggaagca gacaaagcgg tccaagggtt ccacactggg gtccaccagg 500

ctgggaagga agcagagaaa cttggccaag ggggtcaacca tgctgctgac 550

caggctggaa aggaagtgga gaagcttggc caaggtgcc accatgctgc 600

tggccaggcc gggaaggagc tgcagaatgc tcataatggg gtcaaccaag 650  
 ccagcaagga ggccaaccag ctgctgaatg gcaaccatca aagcggatct 700  
 tccagccatc aaggaggggc cacaaccacg ccgttagcct ctgggggcctc 750  
 agtcaacacg cctttcatca accttcccgc cctgtggagg agcgtcgcca 800  
 acatcatgcc ctaaactggc atccggcctt gctgggagaa taatgtcgcc 850  
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<211> 247

<212> PRT

<213> Homo sapiens

<400> 248

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Leu	Gly	Ala	Leu	Ser	Gly	Trp	Ala	Ala	Ser	Asp	Asp	Pro	Ile	Glu	20	25	30	
Lys	Val	Ile	Glu	Gly	Ile	Asn	Arg	Gly	Leu	Ser	Asn	Ala	Glu	Arg	35	40	45	
Glu	Val	Gly	Lys	Ala	Leu	Asp	Gly	Ile	Asn	Ser	Gly	Ile	Thr	His	50	55	60	
Ala	Gly	Arg	Glu	Val	Glu	Lys	Val	Phe	Asn	Gly	Leu	Ser	Asn	Met	65	70	75	
Gly	Ser	His	Thr	Gly	Lys	Glu	Leu	Asp	Lys	Gly	Val	Gln	Gly	Leu	80	85	90	
Asn	His	Gly	Met	Asp	Lys	Val	Ala	His	Glu	Ile	Asn	His	Gly	Ile	95	100	105	
Gly	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	Leu	Gly	His	Gly	Val	Asn	110	115	120	
Asn	Ala	Ala	Gly	Gln	Ala	Gly	Lys	Glu	Ala	Asp	Lys	Ala	Val	Gln	125	130	135	
Gly	Phe	His	Thr	Gly	Val	His	Gln	Ala	Gly	Lys	Glu	Ala	Glu	Lys	140	145	150	
Leu	Gly	Gln	Gly	Val	Asn	His	Ala	Ala	Asp	Gln	Ala	Gly	Lys	Glu	155	160	165	
Val	Glu	Lys	Leu	Gly	Gln	Gly	Ala	His	His	Ala	Ala	Gly	Gln	Ala	170	175	180	



Gly Lys Glu Leu Gln Asn Ala His Asn Gly Val Asn Gln Ala Ser  
185 190 195

Lys Glu Ala Asn Gln Leu Leu Asn Gly Asn His Gln Ser Gly Ser  
200 205 210

Ser Ser His Gln Gly Gly Ala Thr Thr Thr Pro Leu Ala Ser Gly  
215 220 225

Ala Ser Val Asn Thr Pro Phe Ile Asn Leu Pro Ala Leu Trp Arg  
230 235 240

Ser Val Ala Asn Ile Met Pro  
245

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<223> Synthetic construct.

<400> 249  
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<400> 250  
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<223> Synthetic construct.

<400> 251  
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<210> 252  
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<212> DNA  
<213> Homo sapiens



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 <213> Homo sapiens

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 35 40 45  
 Pro Arg Ile Ser Leu Pro Leu Gly Ser Glu Glu Arg Pro Phe Leu  
 50 55 60  
 Arg Phe Glu Ala Glu His Ile Ser Asn Tyr Thr Ala Leu Leu Leu  
 65 70 75  
 Ser Arg Asp Gly Arg Thr Leu Tyr Val Gly Ala Arg Glu Ala Leu

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Phe	Ala	Leu	Ser	Ser	Asn	Leu	Ser	Phe	Leu	Pro	Gly	Gly	Glu	Tyr
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Gln	Glu	Leu	Leu	Trp	Gly	Ala	Asp	Ala	Glu	Lys	Lys	Gln	Gln	Cys
				110					115					120
Ser	Phe	Lys	Gly	Lys	Asp	Pro	Gln	Arg	Asp	Cys	Gln	Asn	Tyr	Ile
				125					130					135
Lys	Ile	Leu	Leu	Pro	Leu	Ser	Gly	Ser	His	Leu	Phe	Thr	Cys	Gly
				140					145					150
Thr	Ala	Ala	Phe	Ser	Pro	Met	Cys	Thr	Tyr	Ile	Asn	Met	Glu	Asn
				155					160					165
Phe	Thr	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Asn	Val	Leu	Leu	Glu	Asp
				170					175					180
Gly	Lys	Gly	Arg	Cys	Pro	Phe	Asp	Pro	Asn	Phe	Lys	Ser	Thr	Ala
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Leu	Val	Val	Asp	Gly	Glu	Leu	Tyr	Thr	Gly	Thr	Val	Ser	Ser	Phe
				200					205					210
Gln	Gly	Asn	Asp	Pro	Ala	Ile	Ser	Arg	Ser	Gln	Ser	Leu	Arg	Pro
				215					220					225
Thr	Lys	Thr	Glu	Ser	Ser	Leu	Asn	Trp	Leu	Gln	Asp	Pro	Ala	Phe
				230					235					240
Val	Ala	Ser	Ala	Tyr	Ile	Pro	Glu	Ser	Leu	Gly	Ser	Leu	Gln	Gly
				245					250					255
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Ser	Glu	Thr	Gly	Gln	Glu
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Phe	Glu	Phe	Phe	Glu	Asn	Thr	Ile	Val	Ser	Arg	Ile	Ala	Arg	Ile
				275					280					285
Cys	Lys	Gly	Asp	Glu	Gly	Gly	Glu	Arg	Val	Leu	Gln	Gln	Arg	Trp
				290					295					300
Thr	Ser	Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Ser	Arg	Pro	Asp	Asp
				305					310					315
Gly	Phe	Pro	Phe	Asn	Val	Leu	Gln	Asp	Val	Phe	Thr	Leu	Ser	Pro
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Ser	Pro	Gln	Asp	Trp	Arg	Asp	Thr	Leu	Phe	Tyr	Gly	Val	Phe	Thr
				335					340					345
Ser	Gln	Trp	His	Arg	Gly	Thr	Thr	Glu	Gly	Ser	Ala	Val	Cys	Val
				350					355					360
Phe	Thr	Met	Lys	Asp	Val	Gln	Arg	Val	Phe	Ser	Gly	Leu	Tyr	Lys
				365					370					375

Glu Val Asn Arg	Glu Thr Gln Gln Trp	Tyr Thr Val Thr His	Pro
380	385		390
Val Pro Thr Pro	Arg Pro Gly Ala Cys	Ile Thr Asn Ser Ala	Arg
395	400		405
Glu Arg Lys Ile	Asn Ser Ser Leu Gln	Leu Pro Asp Arg Val	Leu
410	415		420
Asn Phe Leu Lys	Asp His Phe Leu Met	Asp Gly Gln Val Arg	Ser
425	430		435
Arg Met Leu Leu	Leu Gln Pro Gln Ala	Arg Tyr Gln Arg Val	Ala
440	445		450
Val His Arg Val	Pro Gly Leu His His	Thr Tyr Asp Val Leu	Phe
455	460		465
Leu Gly Thr Gly	Asp Gly Arg Leu His	Lys Ala Val Ser Val	Gly
470	475		480
Pro Arg Val His	Ile Ile Glu Glu Leu	Gln Ile Phe Ser Ser	Gly
485	490		495
Gln Pro Val Gln	Asn Leu Leu Leu Asp	Thr His Arg Gly Leu	Leu
500	505		510
Tyr Ala Ala Ser	His Ser Gly Val Val	Gln Val Pro Met Ala	Asn
515	520		525
Cys Ser Leu Tyr	Arg Ser Cys Gly Asp	Cys Leu Leu Ala Arg	Asp
530	535		540
Pro Tyr Cys Ala	Trp Ser Gly Ser Ser	Cys Lys His Val Ser	Leu
545	550		555
Tyr Gln Pro Gln	Leu Ala Thr Arg Pro	Trp Ile Gln Asp Ile	Glu
560	565		570
Gly Ala Ser Ala	Lys Asp Leu Cys Ser	Ala Ser Ser Val Val	Ser
575	580		585
Pro Ser Phe Val	Pro Thr Gly Glu Lys	Pro Cys Glu Gln Val	Gln
590	595		600
Phe Gln Pro Asn	Thr Val Asn Thr Leu	Ala Cys Pro Leu Leu	Ser
605	610		615
Asn Leu Ala Thr	Arg Leu Trp Leu Arg	Asn Gly Ala Pro Val	Asn
620	625		630
Ala Ser Ala Ser	Cys His Val Leu Pro	Thr Gly Asp Leu Leu	Leu
635	640		645
Val Gly Thr Gln	Gln Leu Gly Glu Phe	Gln Cys Trp Ser Leu	Glu
650	655		660
Glu Gly Phe Gln	Gln Leu Val Ala Ser	Tyr Cys Pro Glu Val	Val

665	670	675
Glu Asp Gly Val	Ala Asp Gln Thr Asp	Glu Gly Gly Ser Val Pro
680	685	690
Val Ile Ile Ser	Thr Ser Arg Val Ser	Ala Pro Ala Gly Gly Lys
695	700	705
Ala Ser Trp Gly	Ala Asp Arg Ser Tyr	Trp Lys Glu Phe Leu Val
710	715	720
Met Cys Thr Leu	Phe Val Leu Ala Val	Leu Leu Pro Val Leu Phe
725	730	735
Leu Leu Tyr Arg	His Arg Asn Ser Met	Lys Val Phe Leu Lys Gln
740	745	750
Gly Glu Cys Ala	Ser Val His Pro Lys	Thr Cys Pro Val Val Leu
755	760	765
Pro Pro Glu Thr	Arg Pro Leu Asn Gly	Leu Gly Pro Pro Ser Thr
770	775	780
Pro Leu Asp His	Arg Gly Tyr Gln Ser	Leu Ser Asp Ser Pro Pro
785	790	795
Gly Ala Arg Val	Phe Thr Glu Ser Glu	Lys Arg Pro Leu Ser Ile
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Gln Asp Ser Phe	Val Glu Val Ser Pro	Val Cys Pro Arg Pro Arg
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Val Arg Leu Gly	Ser Glu Ile Arg Asp	Ser Val Val
830	835	

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<223> Synthetic construct.

<400> 258  
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<210> 259  
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<213> Homo sapiens

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aaacacgaaa aaa 4563

<210> 260

<211> 802

<212> PRT

<213> Homo sapiens

<400> 260

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Leu Val Leu Gly Phe Val Leu Ala Ser Arg Leu Val Leu Pro Arg  
20 25 30

Ala Ser Glu Leu Lys Arg Ala Gly Pro Arg Arg Arg Ala Ser Pro  
35 40 45

Glu Gly Cys Arg Ser Gly Gln Ala Ala Ala Ser Gln Ala Gly Gly  
50 55 60

Ala Arg Gly Asp Ala Arg Gly Ala Gln Leu Trp Pro Pro Gly Ser  
65 70 75

Asp Pro Asp Gly Gly Pro Arg Asp Arg Asn Phe Leu Phe Val Gly  
80 85 90

Val Met Thr Ala Gln Lys Tyr Leu Gln Thr Arg Ala Val Ala Ala  
95 100 105

Tyr Arg Thr Trp Ser Lys Thr Ile Pro Gly Lys Val Gln Phe Phe  
110 115 120

Ser Ser Glu Gly Ser Asp Thr Ser Val Pro Ile Pro Val Val Pro  
125 130 135

Leu Arg Gly Val Asp Asp Ser Tyr Pro Pro Gln Lys Lys Ser Phe  
140 145 150

Met Met Leu Lys Tyr Met His Asp His Tyr Leu Asp Lys Tyr Glu  
155 160 165

Trp Phe Met Arg Ala Asp Asp Asp Val Tyr Ile Lys Gly Asp Arg  
170 175 180

Leu Glu Asn Phe Leu Arg Ser Leu Asn Ser Ser Glu Pro Leu Phe  
185 190 195

Leu Gly Gln Thr Gly Leu Gly Thr Thr Glu Glu Met Gly Lys Leu  
200 205 210

Ala Leu Glu Pro Gly Glu Asn Phe Cys Met Gly Gly Pro Gly Val  
215 220 225

Ile Met Ser Arg Glu Val Leu Arg Arg Met Val Pro His Ile Gly  
230 235 240

FOOTNOTES

Lys Cys Leu Arg	Glu Met Tyr Thr Thr	His Glu Asp Val Glu Val	245	250	255
Gly Arg Cys Val	Arg Arg Phe Ala Gly	Val Gln Cys Val Trp Ser	260	265	270
Tyr Glu Met Arg	Gln Leu Phe Tyr Glu	Asn Tyr Glu Gln Asn Lys	275	280	285
Lys Gly Tyr Ile	Arg Asp Leu His Asn	Ser Lys Ile His Gln Ala	290	295	300
Ile Thr Leu His	Pro Asn Lys Asn Pro	Pro Tyr Gln Tyr Arg Leu	305	310	315
His Ser Tyr Met	Leu Ser Arg Lys Ile	Ser Glu Leu Arg His Arg	320	325	330
Thr Ile Gln Leu	His Arg Glu Ile Val	Leu Met Ser Lys Tyr Ser	335	340	345
Asn Thr Glu Ile	His Lys Glu Asp Leu	Gln Leu Gly Ile Pro Pro	350	355	360
Ser Phe Met Arg	Phe Gln Pro Arg Gln	Arg Glu Glu Ile Leu Glu	365	370	375
Trp Glu Phe Leu	Thr Gly Lys Tyr Leu	Tyr Ser Ala Val Asp Gly	380	385	390
Gln Pro Pro Arg	Arg Gly Met Asp Ser	Ala Gln Arg Glu Ala Leu	395	400	405
Asp Asp Ile Val	Met Gln Val Met Glu	Met Ile Asn Ala Asn Ala	410	415	420
Lys Thr Arg Gly	Arg Ile Ile Asp Phe	Lys Glu Ile Gln Tyr Gly	425	430	435
Tyr Arg Arg Val	Asn Pro Met Tyr Gly	Ala Glu Tyr Ile Leu Asp	440	445	450
Leu Leu Leu Leu	Tyr Lys Lys His Lys	Gly Lys Lys Met Thr Val	455	460	465
Pro Val Arg Arg	His Ala Tyr Leu Gln	Gln Thr Phe Ser Lys Ile	470	475	480
Gln Phe Val Glu	His Glu Glu Leu Asp	Ala Gln Glu Leu Ala Lys	485	490	495
Arg Ile Asn Gln	Glu Ser Gly Ser Leu	Ser Phe Leu Ser Asn Ser	500	505	510
Leu Lys Lys Leu	Val Pro Phe Gln Leu	Pro Gly Ser Lys Ser Glu	515	520	525
His Lys Glu Pro	Lys Asp Lys Lys Ile	Asn Ile Leu Ile Pro Leu			

	530		535		540
Ser Gly Arg Phe	Asp Met Phe Val Arg	Phe Met Gly Asn Phe	Glu		
	545	550	555		
Lys Thr Cys Leu	Ile Pro Asn Gln Asn	Val Lys Leu Val Val	Leu		
	560	565	570		
Leu Phe Asn Ser	Asp Ser Asn Pro Asp	Lys Ala Lys Gln Val	Glu		
	575	580	585		
Leu Met Arg Asp	Tyr Arg Ile Lys Tyr	Pro Lys Ala Asp Met	Gln		
	590	595	600		
Ile Leu Pro Val	Ser Gly Glu Phe Ser	Arg Ala Leu Ala Leu	Glu		
	605	610	615		
Val Gly Ser Ser	Gln Phe Asn Asn Glu	Ser Leu Leu Phe Phe	Cys		
	620	625	630		
Asp Val Asp Leu	Val Phe Thr Thr Glu	Phe Leu Gln Arg Cys	Arg		
	635	640	645		
Ala Asn Thr Val	Leu Gly Gln Gln Ile	Tyr Phe Pro Ile Ile	Phe		
	650	655	660		
Ser Gln Tyr Asp	Pro Lys Ile Val Tyr	Ser Gly Lys Val Pro	Ser		
	665	670	675		
Asp Asn His Phe	Ala Phe Thr Gln Lys	Thr Gly Phe Trp Arg	Asn		
	680	685	690		
Tyr Gly Phe Gly	Ile Thr Cys Ile Tyr	Lys Gly Asp Leu Val	Arg		
	695	700	705		
Val Gly Gly Phe	Asp Val Ser Ile Gln	Gly Trp Gly Leu Glu	Asp		
	710	715	720		
Val Asp Leu Phe	Asn Lys Val Val Gln	Ala Gly Leu Lys Thr	Phe		
	725	730	735		
Arg Ser Gln Glu	Val Gly Val Val His	Val His His Pro Val	Phe		
	740	745	750		
Cys Asp Pro Asn	Leu Asp Pro Lys Gln	Tyr Lys Met Cys Leu	Gly		
	755	760	765		
Ser Lys Ala Ser	Thr Tyr Gly Ser Thr	Gln Gln Leu Ala Glu	Met		
	770	775	780		
Trp Leu Glu Lys	Asn Asp Pro Ser Tyr	Ser Lys Ser Ser Asn	Asn		
	785	790	795		
Asn Gly Ser Val	Arg Thr Ala				
	800				

<210> 261  
<211> 24

<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 261  
gtgccactac ggggtgtgga cgac 24

<210> 262  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 262  
tcccatttct tccgtggtgc ccag 24

<210> 263  
<211> 46  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-46  
<223> Synthetic construct.

<400> 263  
ccagaagaag tccttcatga tgctcaagta catgcacgac cactac 46

<210> 264  
<211> 1419  
<212> DNA  
<213> Homo sapiens

<400> 264  
ggacaaccgt tgctgggtgt cccagggcct gaggcaggac ggtactccgc 50  
tgacaccttc ctttcggcc ttgaggttcc cagcctggtg gccccaggac 100  
gttccggtcg catggcagag tgctacggac gacgcctatg aagcccttag 150  
tccttctagt tgcgcttttg ctatggcctt cgtctgtgcc ggcttatccg 200  
agcataactg tgacacctga tgaagagcaa aacttgaatc attatataca 250  
agtttttagag aacctagtac gaagtgttcc ctctggggag ccaggtcgtg 300  
agaaaaaatc taactctcca aaacatgttt attctatagc atcaaaggga 350  
tcaaaattta aggagctagt tacacatgga gacgcttcaa ctgagaatga 400

tggtttaacc aatcctatca gtgaagaaac tacaactttc cctacaggag 450  
gcttcacacc ggaaatagga aagaaaaaac acacggaaag taccacattc 500  
tggtcgatca aaccaaacia tggtttccatt gttttgcatg cagaggaacc 550  
ttatatgaa aatgaagagc cagagccaga gccggagcca gctgcaaaac 600  
aaactgaggc accaagaatg ttgccagttg ttactgaatc atctacaagt 650  
ccatatgtta cctcatacaa gtcacctgtc accactttag ataagagcac 700  
tggcattgag atctctacag aatcagaaga tggtcctcag ctctcaggtg 750  
aaactgcatg agaaaaaccc gaagagtttg gaaagcacc agagagtttg 800  
aataatgatg acattttgaa aaaaatttta gatattaatt cacaagtgc 850  
acaggcactt cttagtgcac ccagcaaccc agcatataga gaagatattg 900  
aagcctctaa agatcaccta aaacgaagcc ttgctctagc agcagcagca 950  
gaacataaat taaaaacaat gtataagtc cagttattgc cagtaggacg 1000  
aacaagtaat aaaattgatg acatcgaaac tggtattaac atgctgtgta 1050  
attctagatc taaactctat gaatatattg atattaaatg tggtccacca 1100  
gagatgagag aaaaagctgc tacagtattc aatacattaa aaaatatgtg 1150  
tagatcaagg agagtcacag ccttattaaa agtttattaa acaataatat 1200  
aaaaatttta aacctacttg atattccata acaaagctga tttaagcaaa 1250  
ctgcattttt tcacaggaga aataatcata ttcgtaattt caaaagttgt 1300  
ataaaaaatat tttctattgt agttcaaagtg tgccaacatc tttatgtgtc 1350  
atgtgttatg aacaattttc atatgcacta aaaaccta ataaaaataa 1400  
atgttggttc aggaaaaaa 1419

<210> 265  
<211> 350  
<212> PRT  
<213> Homo sapiens

<400> 265  
Met Lys Pro Leu Val Leu Leu Val Ala Leu Leu Leu Trp Pro Ser  
1 5 10 15  
Ser Val Pro Ala Tyr Pro Ser Ile Thr Val Thr Pro Asp Glu Glu  
20 25 30  
Gln Asn Leu Asn His Tyr Ile Gln Val Leu Glu Asn Leu Val Arg  
35 40 45  
Ser Val Pro Ser Gly Glu Pro Gly Arg Glu Lys Lys Ser Asn Ser



	50		55		60
Pro Lys His Val Tyr	Ser Ile Ala Ser Lys Gly Ser Lys Phe Lys				
	65		70		75
Glu Leu Val Thr His	Gly Asp Ala Ser Thr Glu Asn Asp Val Leu				
	80		85		90
Thr Asn Pro Ile Ser	Glu Glu Thr Thr Thr Phe Pro Thr Gly Gly				
	95		100		105
Phe Thr Pro Glu Ile	Gly Lys Lys Lys His Thr Glu Ser Thr Pro				
	110		115		120
Phe Trp Ser Ile Lys	Pro Asn Asn Val Ser Ile Val Leu His Ala				
	125		130		135
Glu Glu Pro Tyr Ile	Glu Asn Glu Glu Pro Glu Pro Glu Pro Glu				
	140		145		150
Pro Ala Ala Lys Gln	Thr Glu Ala Pro Arg Met Leu Pro Val Val				
	155		160		165
Thr Glu Ser Ser Thr	Ser Pro Tyr Val Thr Ser Tyr Lys Ser Pro				
	170		175		180
Val Thr Thr Leu Asp	Lys Ser Thr Gly Ile Glu Ile Ser Thr Glu				
	185		190		195
Ser Glu Asp Val Pro	Gln Leu Ser Gly Glu Thr Ala Ile Glu Lys				
	200		205		210
Pro Glu Glu Phe Gly	Lys His Pro Glu Ser Trp Asn Asn Asp Asp				
	215		220		225
Ile Leu Lys Lys Ile	Leu Asp Ile Asn Ser Gln Val Gln Gln Ala				
	230		235		240
Leu Leu Ser Asp Thr	Ser Asn Pro Ala Tyr Arg Glu Asp Ile Glu				
	245		250		255
Ala Ser Lys Asp His	Leu Lys Arg Ser Leu Ala Leu Ala Ala Ala				
	260		265		270
Ala Glu His Lys Leu	Lys Thr Met Tyr Lys Ser Gln Leu Leu Pro				
	275		280		285
Val Gly Arg Thr Ser	Asn Lys Ile Asp Asp Ile Glu Thr Val Ile				
	290		295		300
Asn Met Leu Cys Asn	Ser Arg Ser Lys Leu Tyr Glu Tyr Leu Asp				
	305		310		315
Ile Lys Cys Val Pro	Pro Glu Met Arg Glu Lys Ala Ala Thr Val				
	320		325		330
Phe Asn Thr Leu Lys	Asn Met Cys Arg Ser Arg Arg Val Thr Ala				
	335		340		345

Leu Leu Lys Val Tyr  
350

<210> 266  
<211> 2403  
<212> DNA  
<213> Homo sapiens

<400> 266  
cggctcgagc ggctcgagtg aagagcctct ccacggctcc tgcgcctgag 50  
acagctggcc tgacctcaa atcatccatc caccctgct gtcattgtt 100  
ttcatagtgt gagatcaacc cacaggaata tccatggctt ttgtgctcat 150  
tttggttctc agtttctacg agctgggtgc aggacagtgg caagtcaactg 200  
gaccgggcaa gtttgtccag gccttggtgg gggaggacgc cgtgttctcc 250  
tgctccctct ttctgagac cagtgcagag gctatggaag tgcggttctt 300  
caggaatcag ttccatgctg tgggtccact ctacagagat ggggaagact 350  
gggaatctaa gcagatgcca cagtatcgag ggagaactga gtttgtgaag 400  
gactccattg caggggggag tgtctctcta aggctaaaaa acatcactcc 450  
ctcggacatc ggctgtatg ggtgctggtt cagttcccag atttacgatg 500  
aggaggccac ctgggagctg cgggtggcag cactgggctc acttcctctc 550  
atttccatcg tgggatatgt tgacggaggt atccagttac tctgcctgtc 600  
ctcaggctgg tttccccagc ccacagccaa gtggaaaggt ccacaaggac 650  
aggatttgtc ttcagactcc agagcaaagt cagatgggta cagcctgtat 700  
gatgtggaga tctccattat agtccaggaa aatgctggga gcatattgtg 750  
ttccatccac cttgctgagc agagtcattg ggtggaatcc aaggtattga 800  
taggagagac gtttttccag cctcaccctt ggcgctggc ttctatttta 850  
ctcgggttac tctgtggtgc cctgtgtggt gttgtcatgg ggatgataat 900  
tgttttcttc aaatccaaag ggaaaatoca ggcggaactg gactggagaa 950  
gaaagcacgg acaggcagaa ttgagagacg cccggaaaca cgcagtggag 1000  
gtgactctgg atccagagac ggctcaccog aagctctgag tttctgatct 1050  
gaaaactgta acccatagaa aagctcccca ggaggtgcct cactctgaga 1100  
agagatttac aaggaagagt gtggtggctt ctcagggttt ccaagcaggg 1150  
agacattact gggaggtgga cgtgggacaa aatgtagggt ggtatgtggg 1200  
agtgtgtcgg gatgacgtag acagggggaa gaacaatgtg actttgtctc 1250

ccaacaatgg gtattgggtc ctcagactga caacagaaca tttgtatttc 1300  
acattcaatc cccattttat cagcctcccc cccagcaccc ctcctacacg 1350  
agtaggggtc ttcctggact atgaggggtg gaccatctcc ttcttcaata 1400  
caaatgacca gtcccttatt tataccctgc tgacatgtca gtttgaaggc 1450  
ttgttgagac cctatatcca gcatgcatg tatgacgagg aaaaggggac 1500  
tcccatattc atatgtccag tgcctgggg atgagacaga gaagaccctg 1550  
cttaaagggc cccacaccac agaccagac acagccaagg gagagtgtc 1600  
ccgacaggtg gccccagctt cctctccgga gcctgcatc agagagtcac 1650  
gcccccaact ctcctttagg gagctgaggt tcttctgccc tgagccctgc 1700  
agcagcggca gtcacagctt ccagatgagg ggggattggc ctgaccctgt 1750  
gggagtcaga agccatggct gcctgaagt ggggacggaa tagactcaca 1800  
ttaggtttag tttgtgaaaa ctccatccag ctaagcgatc ttgaacaagt 1850  
cacaacctcc caggctcctc atttgctagt cacggacagt gattcctgcc 1900  
tcacaggtga agattaaaga gacaacgaat gtgaatcatg cttgcagggt 1950  
tgagggcaca gtgtttgcta atgatgtgtt tttatattat acattttccc 2000  
accataaact ctgtttgctt attccacatt aatttacttt tctctatacc 2050  
aaatcaccca tggaatagtt attgaacacc tgctttgtga ggctcaaaga 2100  
ataaagagga ggtaggattt ttactgatt ctataagccc agcattacct 2150  
gataccaaaa ccaggcaaag aaaacagaag aagaggaagg aaaactacag 2200  
gtccatatcc ctcattaaca cagacacaaa aattctaat aaaattttaa 2250  
caaattaaac taaacaatat atttaaagat gatataaac tactcagtgt 2300  
ggtttgtccc acaaatgcag agttgggtta atatttaaat atcaaccagt 2350  
gtaattcagc acattaataa agtaaaaaag aaaaccataa aaaaaaaaaa 2400  
aaa 2403

<210> 267  
<211> 466  
<212> PRT  
<213> Homo sapiens

<400> 267  
Met Ala Phe Val Leu Ile Leu Val Leu Ser Phe Tyr Glu Leu Val  
1 5 10 15  
Ser Gly Gln Trp Gln Val Thr Gly Pro Gly Lys Phe Val Gln Ala

20					25					30				
Leu	Val	Gly	Glu	Asp	Ala	Val	Phe	Ser	Cys	Ser	Leu	Phe	Pro	Glu
				35					40					45
Thr	Ser	Ala	Glu	Ala	Met	Glu	Val	Arg	Phe	Phe	Arg	Asn	Gln	Phe
				50					55					60
His	Ala	Val	Val	His	Leu	Tyr	Arg	Asp	Gly	Glu	Asp	Trp	Glu	Ser
				65					70					75
Lys	Gln	Met	Pro	Gln	Tyr	Arg	Gly	Arg	Thr	Glu	Phe	Val	Lys	Asp
				80					85					90
Ser	Ile	Ala	Gly	Gly	Arg	Val	Ser	Leu	Arg	Leu	Lys	Asn	Ile	Thr
				95					100					105
Pro	Ser	Asp	Ile	Gly	Leu	Tyr	Gly	Cys	Trp	Phe	Ser	Ser	Gln	Ile
				110					115					120
Tyr	Asp	Glu	Glu	Ala	Thr	Trp	Glu	Leu	Arg	Val	Ala	Ala	Leu	Gly
				125					130					135
Ser	Leu	Pro	Leu	Ile	Ser	Ile	Val	Gly	Tyr	Val	Asp	Gly	Gly	Ile
				140					145					150
Gln	Leu	Leu	Cys	Leu	Ser	Ser	Gly	Trp	Phe	Pro	Gln	Pro	Thr	Ala
				155					160					165
Lys	Trp	Lys	Gly	Pro	Gln	Gly	Gln	Asp	Leu	Ser	Ser	Asp	Ser	Arg
				170					175					180
Ala	Asn	Ala	Asp	Gly	Tyr	Ser	Leu	Tyr	Asp	Val	Glu	Ile	Ser	Ile
				185					190					195
Ile	Val	Gln	Glu	Asn	Ala	Gly	Ser	Ile	Leu	Cys	Ser	Ile	His	Leu
				200					205					210
Ala	Glu	Gln	Ser	His	Glu	Val	Glu	Ser	Lys	Val	Leu	Ile	Gly	Glu
				215					220					225
Thr	Phe	Phe	Gln	Pro	Ser	Pro	Trp	Arg	Leu	Ala	Ser	Ile	Leu	Leu
				230					235					240
Gly	Leu	Leu	Cys	Gly	Ala	Leu	Cys	Gly	Val	Val	Met	Gly	Met	Ile
				245					250					255
Ile	Val	Phe	Phe	Lys	Ser	Lys	Gly	Lys	Ile	Gln	Ala	Glu	Leu	Asp
				260					265					270
Trp	Arg	Arg	Lys	His	Gly	Gln	Ala	Glu	Leu	Arg	Asp	Ala	Arg	Lys
				275					280					285
His	Ala	Val	Glu	Val	Thr	Leu	Asp	Pro	Glu	Thr	Ala	His	Pro	Lys
				290					295					300
Leu	Cys	Val	Ser	Asp	Leu	Lys	Thr	Val	Thr	His	Arg	Lys	Ala	Pro
				305					310					315

Gln Glu Val Pro His Ser Glu Lys Arg Phe Thr Arg Lys Ser Val  
 320 325 330

Val Ala Ser Gln Gly Phe Gln Ala Gly Arg His Tyr Trp Glu Val  
 335 340 345

Asp Val Gly Gln Asn Val Gly Trp Tyr Val Gly Val Cys Arg Asp  
 350 355 360

Asp Val Asp Arg Gly Lys Asn Asn Val Thr Leu Ser Pro Asn Asn  
 365 370 375

Gly Tyr Trp Val Leu Arg Leu Thr Thr Glu His Leu Tyr Phe Thr  
 380 385 390

Phe Asn Pro His Phe Ile Ser Leu Pro Pro Ser Thr Pro Pro Thr  
 395 400 405

Arg Val Gly Val Phe Leu Asp Tyr Glu Gly Gly Thr Ile Ser Phe  
 410 415 420

Phe Asn Thr Asn Asp Gln Ser Leu Ile Tyr Thr Leu Leu Thr Cys  
 425 430 435

Gln Phe Glu Gly Leu Leu Arg Pro Tyr Ile Gln His Ala Met Tyr  
 440 445 450

Asp Glu Glu Lys Gly Thr Pro Ile Phe Ile Cys Pro Val Ser Trp  
 455 460 465

Gly

<210> 268  
 <211> 2103  
 <212> DNA  
 <213> Homo sapiens

<400> 268  
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 tggtgagggc taggaaaaga gtttggttggg aaccctgggt tatcggcctc 100  
 gtcattctca tatccctgat tgtcctggca gtgtgcattg gactcactgt 150  
 tcattatgtg agatataatc aaaagaagac ctacaattac tatagcacat 200  
 tgtcatttac aactgacaaa ctatatgctg agtttggcag agaggcttct 250  
 aacaatttta cagaaatgag ccagagactt gaatcaatgg tgaaaaatgc 300  
 attttataaa tctccattaa gggaagaatt tgtcaagtct caggttatca 350  
 agttcagtca acagaagcat ggagtgttgg ctcatatgct gttgatttgt 400  
 agatttcact ctactgagga tcctgaaact gtagataaaa ttgttcaact 450  
 tgttttacat gaaaagctgc aagatgctgt aggaccccct aaagtagatc 500

ctcactcagt taaaattaaa aaaatcaaca agacagaaac agacagctat 550  
ctaaaccatt gctgcggaac acgaagaagt aaaactctag gtcagagtct 600  
caggatcggt ggtgggacag aagtagaaga gggatgaatgg ccctggcagg 650  
ctagcctgca gtgggatggg agtcatcgct gtggagcaac ctttaattaat 700  
gccacatggc ttgtgagtgc tgctcactgt tttaacaacat ataagaaccc 750  
tgccagatgg actgcttcct ttggagtaac aataaaacct tcgaaaatga 800  
aacgggggtct ccggagaata attgtccatg aaaaatacaa acacccatca 850  
catgactatg atattttctct tgcagagctt tctagccctg ttccctacac 900  
aaatgcagta catagagttt gtctccctga tgcctcctat gagtttcaac 950  
caggtgatgt gatgtttgtg acaggatttg gagcactgaa aaatgatggg 1000  
tacagtcaaa atcatcttcg acaagcacag gtgactctca tagacgctac 1050  
aacttgcaat gaacctcaag cttacaatga cgccataact cctagaatgt 1100  
tatgtgctgg ctcccttagaa ggaaaaacag atgcatgccg gggtgactct 1150  
ggaggaccac tggtagttc agatgctaga gatctctggg accttgctgg 1200  
aatagtgagc tggggagatg aatgtgcgaa acccaacaag cctgggtgtt 1250  
atactagagt tacggccttg cgggactgga ttacttcaaa aactgggtatc 1300  
taagagacaa aagcctcatg gaacagataa cttttttttt tgttttttgg 1350  
gtgtggaggc cttttttaga gatacagaat tggagaagac ttgcaaaaca 1400  
gctagatttg actgatctca ataaactgtt tgcttgatgc atgtattttc 1450  
ttcccagctc tgttccgcac gtaagcatcc tgcttctgcc agatcaactc 1500  
tgtcatctgt gagcaatagt tgaaacttta tgtacataga gaaatagata 1550  
atacaatatt acattacagc ctgtattcat ttgttctcta gaagttttgt 1600  
cagaattttg acttggtgac ataaatttgt aatgcatata tacaatttga 1650  
agcactcctt ttcttcagtt cctcagctcc tctcatttca gcaaatatcc 1700  
attttcaagg tgcagaacaa ggagtgaag aaaatataag aagaaaaaaa 1750  
tcccctacat ttatttgga cagaaaagta ttaggtgtt ttcttagtgg 1800  
aatattagaa atgatcatat tcattatgaa aggtcaagca aagacagcag 1850  
aataccaatc acttcatcat ttaggaagta tgggaactaa gttaaggaag 1900  
tccagaaaga agccaagata tatccttatt ttcatttcca aacaactact 1950

atgataaatg tgaagaagat tctgtttttt tgtgacctat aataattata 2000  
 caaacttcat gcaatgtact tgttotaagc aaattaaagc aaatatttat 2050  
 ttaacattgt tactgaggat gtcaacatat aacaataaaa tataaatcac 2100  
 cca 2103

<210> 269  
 <211> 423  
 <212> PRT  
 <213> Homo sapiens

<400> 269  
 Met Met Tyr Arg Pro Asp Val Val Arg Ala Arg Lys Arg Val Cys  
   1                  5                  10                  15  
 Trp Glu Pro Trp Val Ile Gly Leu Val Ile Phe Ile Ser Leu Ile  
                   20                  25                  30  
 Val Leu Ala Val Cys Ile Gly Leu Thr Val His Tyr Val Arg Tyr  
                   35                  40                  45  
 Asn Gln Lys Lys Thr Tyr Asn Tyr Tyr Ser Thr Leu Ser Phe Thr  
                   50                  55                  60  
 Thr Asp Lys Leu Tyr Ala Glu Phe Gly Arg Glu Ala Ser Asn Asn  
                   65                  70                  75  
 Phe Thr Glu Met Ser Gln Arg Leu Glu Ser Met Val Lys Asn Ala  
                   80                  85                  90  
 Phe Tyr Lys Ser Pro Leu Arg Glu Glu Phe Val Lys Ser Gln Val  
                   95                  100                  105  
 Ile Lys Phe Ser Gln Gln Lys His Gly Val Leu Ala His Met Leu  
                   110                  115                  120  
 Leu Ile Cys Arg Phe His Ser Thr Glu Asp Pro Glu Thr Val Asp  
                   125                  130                  135  
 Lys Ile Val Gln Leu Val Leu His Glu Lys Leu Gln Asp Ala Val  
                   140                  145                  150  
 Gly Pro Pro Lys Val Asp Pro His Ser Val Lys Ile Lys Lys Ile  
                   155                  160                  165  
 Asn Lys Thr Glu Thr Asp Ser Tyr Leu Asn His Cys Cys Gly Thr  
                   170                  175                  180  
 Arg Arg Ser Lys Thr Leu Gly Gln Ser Leu Arg Ile Val Gly Gly  
                   185                  190                  195  
 Thr Glu Val Glu Glu Gly Glu Trp Pro Trp Gln Ala Ser Leu Gln  
                   200                  205                  210  
 Trp Asp Gly Ser His Arg Cys Gly Ala Thr Leu Ile Asn Ala Thr  
                   215                  220                  225

Trp	Leu	Val	Ser	Ala	Ala	His	Cys	Phe	Thr	Thr	Tyr	Lys	Asn	Pro
				230					235					240
Ala	Arg	Trp	Thr	Ala	Ser	Phe	Gly	Val	Thr	Ile	Lys	Pro	Ser	Lys
				245					250					255
Met	Lys	Arg	Gly	Leu	Arg	Arg	Ile	Ile	Val	His	Glu	Lys	Tyr	Lys
				260					265					270
His	Pro	Ser	His	Asp	Tyr	Asp	Ile	Ser	Leu	Ala	Glu	Leu	Ser	Ser
				275					280					285
Pro	Val	Pro	Tyr	Thr	Asn	Ala	Val	His	Arg	Val	Cys	Leu	Pro	Asp
				290					295					300
Ala	Ser	Tyr	Glu	Phe	Gln	Pro	Gly	Asp	Val	Met	Phe	Val	Thr	Gly
				305					310					315
Phe	Gly	Ala	Leu	Lys	Asn	Asp	Gly	Tyr	Ser	Gln	Asn	His	Leu	Arg
				320					325					330
Gln	Ala	Gln	Val	Thr	Leu	Ile	Asp	Ala	Thr	Thr	Cys	Asn	Glu	Pro
				335					340					345
Gln	Ala	Tyr	Asn	Asp	Ala	Ile	Thr	Pro	Arg	Met	Leu	Cys	Ala	Gly
				350					355					360
Ser	Leu	Glu	Gly	Lys	Thr	Asp	Ala	Cys	Gln	Gly	Asp	Ser	Gly	Gly
				365					370					375
Pro	Leu	Val	Ser	Ser	Asp	Ala	Arg	Asp	Ile	Trp	Tyr	Leu	Ala	Gly
				380					385					390
Ile	Val	Ser	Trp	Gly	Asp	Glu	Cys	Ala	Lys	Pro	Asn	Lys	Pro	Gly
				395					400					405
Val	Tyr	Thr	Arg	Val	Thr	Ala	Leu	Arg	Asp	Trp	Ile	Thr	Ser	Lys
				410					415					420

Thr Gly Ile

<210> 270  
 <211> 1170  
 <212> DNA  
 <213> Homo sapiens

<400> 270  
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 cagacgtcag ctggtggatt cccgctgcat caaggcctac ccactgtctc 150  
 catgctgggc tctccctgcc ttctgtgggt cctggccgtg accttcttgg 200  
 ttcccagagc tcagcccttg gccctcaag actttgaaga agaggaggca 250



gatgagactg agacggcgtg gccgcctttg ccggctgtcc cctgcgacta 300  
cgaccactgc cgacacctgc aggtgccctg caaggagcta cagaggggtcg 350  
ggccggcggc ctgcctgtgc ccaggactct ccagccccgc ccagccgccc 400  
gacccgcccgc gcatgggaga agtgcgcatc gcggccgaag agggccgctg 450  
agtgggtccac tgggtgtgcc ccttctcccc ggtcctccac tactgggtgc 500  
tgctttggga cggcagcgag gctgcgaga aggggcccc gctgaacgct 550  
acgggtccgca gagccgaact gaaggggctg aagccagggg gcatttatgt 600  
cgtttgcgta gtggccgcta acgaggccgg ggcaagccgc gtgccccagg 650  
ctggaggaga gggcctcgag ggggcccaga tccctgcctt cgggccttgc 700  
agccgccttg cggtgccgcc caacccccgc actctggtcc acgcggccgt 750  
cgggggtgggc acggccctgg cctgtctaag ctgtgccgcc ctgggtgtggc 800  
acttctgcct gcgcgatcgc tggggctgcc cgcgccgagc cgccgcccga 850  
gccgcagggg cgctctgaaa ggggcctggg ggcatctcgg gcacagacag 900  
ccccacctgg ggcgctcagc ctggcccccg ggaaagagga aaacccgctg 950  
cctccaggga gggctggacg gcgagctggg agccagcccc aggctccagg 1000  
gccacggcgg agtcatggtt ctcaggactg agcgcttggt taggtccggt 1050  
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ccccaatttt tttttaagcg gccagataat aaataatgta acctttgcgg 1150  
ttaaaaaaaaa aaaaaaaaaa 1170

<210> 271  
<211> 238  
<212> PRT  
<213> Homo sapiens

<400> 271  
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Leu Val Pro Arg Ala Gln Pro Leu Ala Pro Gln Asp Phe Glu Glu  
20 25 30  
Glu Glu Ala Asp Glu Thr Glu Thr Ala Trp Pro Pro Leu Pro Ala  
35 40 45  
Val Pro Cys Asp Tyr Asp His Cys Arg His Leu Gln Val Pro Cys  
50 55 60  
Lys Glu Leu Gln Arg Val Gly Pro Ala Ala Cys Leu Cys Pro Gly  
65 70 75

Leu	Ser	Ser	Pro	Ala	Gln	Pro	Pro	Asp	Pro	Pro	Arg	Met	Gly	Glu	
				80					85					90	
Val	Arg	Ile	Ala	Ala	Glu	Glu	Gly	Arg	Ala	Val	Val	His	Trp	Cys	
				95					100					105	
Ala	Pro	Phe	Ser	Pro	Val	Leu	His	Tyr	Trp	Leu	Leu	Leu	Trp	Asp	
				110					115					120	
Gly	Ser	Glu	Ala	Ala	Gln	Lys	Gly	Pro	Pro	Leu	Asn	Ala	Thr	Val	
				125					130					135	
Arg	Arg	Ala	Glu	Leu	Lys	Gly	Leu	Lys	Pro	Gly	Gly	Ile	Tyr	Val	
				140					145					150	
Val	Cys	Val	Val	Ala	Ala	Asn	Glu	Ala	Gly	Ala	Ser	Arg	Val	Pro	
				155					160					165	
Gln	Ala	Gly	Gly	Glu	Gly	Leu	Glu	Gly	Ala	Asp	Ile	Pro	Ala	Phe	
				170					175					180	
Gly	Pro	Cys	Ser	Arg	Leu	Ala	Val	Pro	Pro	Asn	Pro	Arg	Thr	Leu	
				185					190					195	
Val	His	Ala	Ala	Val	Gly	Val	Gly	Thr	Ala	Leu	Ala	Leu	Leu	Ser	
				200					205					210	
Cys	Ala	Ala	Leu	Val	Trp	His	Phe	Cys	Leu	Arg	Asp	Arg	Trp	Gly	
				215					220					225	
Cys	Pro	Arg	Arg	Ala	Ala	Ala	Arg	Ala	Ala	Gly	Ala	Leu			
				230					235						

<210> 272  
 <211> 2397  
 <212> DNA  
 <213> Homo sapiens

<400> 272  
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 cccaggcggg cgtggggcac cgggcccagc gccgacgatc gctgccgttt 150  
 tgcccttggg agtaggatgt ggtgaaagga tggggcttct cccttacggg 200  
 gctcacaatg gccagagaag attccgtgaa gtgtctgcgc tgctgtctct 250  
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 cggatcatgat tgctgtttgc tgtttcctta tcattgtggg gatgttagga 450  
 tattgtggaa cggtgaaaag aaatctgttg cttcttgcac ggtactttgg 500

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aaagccagga tgacaaatta tggattacct agatatcggg ggcttactca 650  
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atgacaactc tcagcacctg tcatgtccct cagtagaact gttgaaacca 1050  
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caaacttggt ttattggact tgtgaatddd tgagtacata ctatgtgttt 1200  
cagaaatatg tagaaataaa aatgttgcca taaaataaca cctaagcata 1250  
tactattcta tgcttttaaa tgaggatgga aaagtttcat gtcataagtc 1300  
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accactgtg tagcctgtgt atgactttta ctgaacacag ttatgttttg 1400  
aggcagcatg gtttgattag catttccgca tccatgcaaa cgagtcacat 1450  
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acttttatta ctcagcgatc tattcttctg atgctaaata aattatatat 1600  
cagaaaactt tcaatattgg tgactaccta aatgtgattt ttgctgggta 1650  
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actattctgt cctgggctta tattacacat ataactgtta tttaaatact 1900  
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agaatgtagt ctggtcttta ggaagtatta ataagaaaat ttgcacataa 2000  
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 ctctttttga cactaaacac tttttaaaaa gcttatcttt gccttctcca 2100  
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 ttctttttct ccagaaaaat gcttgtgaga atcattaaaa catgtgacaa 2200  
 tttagagatt ctttgtttta tttcactgat taatatactg tggcaaatta 2250  
 cacagattat taaatTTTTT tacaagagta tagtatattt atttgaaatg 2300  
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<210> 273

<211> 305

<212> PRT

<213> Homo sapiens

<400> 273

Met	Ala	Arg	Glu	Asp	Ser	Val	Lys	Cys	Leu	Arg	Cys	Leu	Leu	Tyr
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Ala	Leu	Asn	Leu	Leu	Phe	Trp	Leu	Met	Ser	Ile	Ser	Val	Leu	Ala
				20					25					30
Val	Ser	Ala	Trp	Met	Arg	Asp	Tyr	Leu	Asn	Asn	Val	Leu	Thr	Leu
				35					40					45
Thr	Ala	Glu	Thr	Arg	Val	Glu	Glu	Ala	Val	Ile	Leu	Thr	Tyr	Phe
				50					55					60
Pro	Val	Val	His	Pro	Val	Met	Ile	Ala	Val	Cys	Cys	Phe	Leu	Ile
				65					70					75
Ile	Val	Gly	Met	Leu	Gly	Tyr	Cys	Gly	Thr	Val	Lys	Arg	Asn	Leu
				80					85					90
Leu	Leu	Leu	Ala	Trp	Tyr	Phe	Gly	Ser	Leu	Leu	Val	Ile	Phe	Cys
				95					100					105
Val	Glu	Leu	Ala	Cys	Gly	Val	Trp	Thr	Tyr	Glu	Gln	Glu	Leu	Met
				110					115					120
Val	Pro	Val	Gln	Trp	Ser	Asp	Met	Val	Thr	Leu	Lys	Ala	Arg	Met
				125					130					135
Thr	Asn	Tyr	Gly	Leu	Pro	Arg	Tyr	Arg	Trp	Leu	Thr	His	Ala	Trp
				140					145					150
Asn	Phe	Phe	Gln	Arg	Glu	Phe	Lys	Cys	Cys	Gly	Val	Val	Tyr	Phe
				155					160					165
Thr	Asp	Trp	Leu	Glu	Met	Thr	Glu	Met	Asp	Trp	Pro	Pro	Asp	Ser

170	175	180
Cys Cys Val Arg Glu Phe Pro Gly Cys Ser Lys Gln Ala His Gln		
185	190	195
Glu Asp Leu Ser Asp Leu Tyr Gln Glu Gly Cys Gly Lys Lys Met		
200	205	210
Tyr Ser Phe Leu Arg Gly Thr Lys Gln Leu Gln Val Leu Arg Phe		
215	220	225
Leu Gly Ile Ser Ile Gly Val Thr Gln Ile Leu Ala Met Ile Leu		
230	235	240
Thr Ile Thr Leu Leu Trp Ala Leu Tyr Tyr Asp Arg Arg Glu Pro		
245	250	255
Gly Thr Asp Gln Met Met Ser Leu Lys Asn Asp Asn Ser Gln His		
260	265	270
Leu Ser Cys Pro Ser Val Glu Leu Leu Lys Pro Ser Leu Ser Arg		
275	280	285
Ile Phe Glu His Thr Ser Met Ala Asn Ser Phe Asn Thr His Phe		
290	295	300
Glu Met Glu Glu Leu		
305		

<210> 274  
 <211> 2063  
 <212> DNA  
 <213> Homo sapiens

<400> 274  
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caaaaaaaaaaaa aaa 2063

<210> 275

<211> 432

<212> PRT

<213> Homo sapiens

<400> 275

Met	Leu	Gln	Asp	Pro	Asp	Ser	Asp	Gln	Pro	Leu	Asn	Ser	Leu	Asp
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Val	Lys	Pro	Leu	Arg	Lys	Pro	Arg	Ile	Pro	Met	Glu	Thr	Phe	Arg
				20					25					30

Lys	Val	Gly	Ile	Pro	Ile	Ile	Ile	Ala	Leu	Leu	Ser	Leu	Ala	Ser
				35					40					45

Ile	Ile	Ile	Val	Val	Val	Leu	Ile	Lys	Val	Ile	Leu	Asp	Lys	Tyr
				50					55					60

Tyr	Phe	Leu	Cys	Gly	Gln	Pro	Leu	His	Phe	Ile	Pro	Arg	Lys	Gln
				65					70					75

Leu	Cys	Asp	Gly	Glu	Leu	Asp	Cys	Pro	Leu	Gly	Glu	Asp	Glu	Glu
				80					85					90

His	Cys	Val	Lys	Ser	Phe	Pro	Glu	Gly	Pro	Ala	Val	Ala	Val	Arg
				95					100					105

Leu	Ser	Lys	Asp	Arg	Ser	Thr	Leu	Gln	Val	Leu	Asp	Ser	Ala	Thr
				110					115					120

Gly	Asn	Trp	Phe	Ser	Ala	Cys	Phe	Asp	Asn	Phe	Thr	Glu	Ala	Leu
				125					130					135

Ala	Glu	Thr	Ala	Cys	Arg	Gln	Met	Gly	Tyr	Ser	Arg	Ala	Val	Glu
				140					145					150

Ile	Gly	Pro	Asp	Gln	Asp	Leu	Asp	Val	Val	Glu	Ile	Thr	Glu	Asn
				155					160					165

Ser	Gln	Glu	Leu	Arg	Met	Arg	Asn	Ser	Ser	Gly	Pro	Cys	Leu	Ser
				170					175					180

Gly	Ser	Leu	Val	Ser	Leu	His	Cys	Leu	Ala	Cys	Gly	Lys	Ser	Leu
				185					190					195

Lys	Thr	Pro	Arg	Val	Val	Gly	Gly	Glu	Glu	Ala	Ser	Val	Asp	Ser
				200					205					210

Trp	Pro	Trp	Gln	Val	Ser	Ile	Gln	Tyr	Asp	Lys	Gln	His	Val	Cys
				215					220					225

Gly	Gly	Ser	Ile	Leu	Asp	Pro	His	Trp	Val	Leu	Thr	Ala	Ala	His
				230					235					240

Cys	Phe	Arg	Lys	His	Thr	Asp	Val	Phe	Asn	Trp	Lys	Val	Arg	Ala
				245					250					255







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taccctgtga tctcctactg ggtggacagc caggaccaga ccctggccct 2050  
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<210> 277

<211> 761

<212> PRT

<213> Homo sapiens

<400> 277

Met	Ala	Leu	Pro	Ala	Leu	Gly	Leu	Asp	Pro	Trp	Ser	Leu	Leu	Gly	1	5	10	15
Leu	Phe	Leu	Phe	Gln	Leu	Leu	Gln	Leu	Leu	Leu	Pro	Thr	Thr	Thr	20	25	30	
Ala	Gly	Gly	Gly	Gly	Gln	Gly	Pro	Met	Pro	Arg	Val	Arg	Tyr	Tyr	35	40	45	
Ala	Gly	Asp	Glu	Arg	Arg	Ala	Leu	Ser	Phe	Phe	His	Gln	Lys	Gly	50	55	60	
Leu	Gln	Asp	Phe	Asp	Thr	Leu	Leu	Leu	Ser	Gly	Asp	Gly	Asn	Thr	65	70	75	
Leu	Tyr	Val	Gly	Ala	Arg	Glu	Ala	Ile	Leu	Ala	Leu	Asp	Ile	Gln	80	85	90	
Asp	Pro	Gly	Val	Pro	Arg	Leu	Lys	Asn	Met	Ile	Pro	Trp	Pro	Ala	95	100	105	
Ser	Asp	Arg	Lys	Lys	Ser	Glu	Cys	Ala	Phe	Lys	Lys	Lys	Ser	Asn	110	115	120	
Glu	Thr	Gln	Cys	Phe	Asn	Phe	Ile	Arg	Val	Leu	Val	Ser	Tyr	Asn	125	130	135	
Val	Thr	His	Leu	Tyr	Thr	Cys	Gly	Thr	Phe	Ala	Phe	Ser	Pro	Ala	140	145	150	
Cys	Thr	Phe	Ile	Glu	Leu	Gln	Asp	Ser	Tyr	Leu	Leu	Pro	Ile	Ser	155	160	165	
Glu	Asp	Lys	Val	Met	Glu	Gly	Lys	Gly	Gln	Ser	Pro	Phe	Asp	Pro	170	175	180	
Ala	His	Lys	His	Thr	Ala	Val	Leu	Val	Asp	Gly	Met	Leu	Tyr	Ser	185	190	195	
Gly	Thr	Met	Asn	Asn	Phe	Leu	Gly	Ser	Glu	Pro	Ile	Leu	Met	Arg	200	205	210	
Thr	Leu	Gly	Ser	Gln	Pro	Val	Leu	Lys	Thr	Asp	Asn	Phe	Leu	Arg	215	220	225	
Trp	Leu	His	His	Asp	Ala	Ser	Phe	Val	Ala	Ala	Ile	Pro	Ser	Thr	230	235	240	
Gln	Val	Val	Tyr	Phe	Phe	Phe	Glu	Glu	Thr	Ala	Ser	Glu	Phe	Asp	245	250	255	
Phe	Phe	Glu	Arg	Leu	His	Thr	Ser	Arg	Val	Ala	Arg	Val	Cys	Lys	260	265	270	
Asn	Asp	Val	Gly	Gly	Glu	Lys	Leu	Leu	Gln	Lys	Lys	Trp	Thr	Thr	275	280	285	
Phe	Leu	Lys	Ala	Gln	Leu	Leu	Cys	Thr	Gln	Pro	Gly	Gln	Leu	Pro				

	290		295		300
Phe Asn Val Ile	Arg 305	His Ala Val Leu	Leu 310	Pro Ala Asp Ser	Pro 315
Thr Ala Pro His	Ile 320	Tyr Ala Val Phe	Thr 325	Ser Gln Trp Gln	Val 330
Gly Gly Thr Arg	Ser 335	Ser Ala Val Cys	Ala 340	Phe Ser Leu Leu	Asp 345
Ile Glu Arg Val	Phe 350	Lys Gly Lys Tyr	Lys 355	Glu Leu Asn Lys	Glu 360
Thr Ser Arg Trp	Thr 365	Thr Tyr Arg Gly	Pro 370	Glu Thr Asn Pro	Arg 375
Pro Gly Ser Cys	Ser 380	Val Gly Pro Ser	Ser 385	Asp Lys Ala Leu	Thr 390
Phe Met Lys Asp	His 395	Phe Leu Met Asp	Glu 400	Gln Val Val Gly	Thr 405
Pro Leu Leu Val	Lys 410	Ser Gly Val Glu	Tyr 415	Thr Arg Leu Ala	Val 420
Glu Thr Ala Gln	Gly 425	Leu Asp Gly His	Ser 430	His Leu Val Met	Tyr 435
Leu Gly Thr Thr	Thr 440	Gly Ser Leu His	Lys 445	Ala Val Val Ser	Gly 450
Asp Ser Ser Ala	His 455	Leu Val Glu Glu	Ile 460	Gln Leu Phe Pro	Asp 465
Pro Glu Pro Val	Arg 470	Asn Leu Gln Leu	Ala 475	Pro Thr Gln Gly	Ala 480
Val Phe Val Gly	Phe 485	Ser Gly Gly Val	Trp 490	Arg Val Pro Arg	Ala 495
Asn Cys Ser Val	Tyr 500	Glu Ser Cys Val	Asp 505	Cys Val Leu Ala	Arg 510
Asp Pro His Cys	Ala 515	Trp Asp Pro Glu	Ser 520	Arg Thr Cys Cys	Leu 525
Leu Ser Ala Pro	Asn 530	Leu Asn Ser Trp	Lys 535	Gln Asp Met Glu	Arg 540
Gly Asn Pro Glu	Trp 545	Ala Cys Ala Ser	Gly 550	Pro Met Ser Arg	Ser 555
Leu Arg Pro Gln	Ser 560	Arg Pro Gln Ile	Ile 565	Lys Glu Val Leu	Ala 570
Val Pro Asn Ser	Ile 575	Leu Glu Leu Pro	Cys 580	Pro His Leu Ser	Ala 585

Leu	Ala	Ser	Tyr	Tyr	Trp	Ser	His	Gly	Pro	Ala	Ala	Val	Pro	Glu
				590					595					600
Ala	Ser	Ser	Thr	Val	Tyr	Asn	Gly	Ser	Leu	Leu	Leu	Ile	Val	Gln
				605					610					615
Asp	Gly	Val	Gly	Gly	Leu	Tyr	Gln	Cys	Trp	Ala	Thr	Glu	Asn	Gly
				620					625					630
Phe	Ser	Tyr	Pro	Val	Ile	Ser	Tyr	Trp	Val	Asp	Ser	Gln	Asp	Gln
				635					640					645
Thr	Leu	Ala	Leu	Asp	Pro	Glu	Leu	Ala	Gly	Ile	Pro	Arg	Glu	His
				650					655					660
Val	Lys	Val	Pro	Leu	Thr	Arg	Val	Ser	Gly	Gly	Ala	Ala	Leu	Ala
				665					670					675
Ala	Gln	Gln	Ser	Tyr	Trp	Pro	His	Phe	Val	Thr	Val	Thr	Val	Leu
				680					685					690
Phe	Ala	Leu	Val	Leu	Ser	Gly	Ala	Leu	Ile	Ile	Leu	Val	Ala	Ser
				695					700					705
Pro	Leu	Arg	Ala	Leu	Arg	Ala	Arg	Gly	Lys	Val	Gln	Gly	Cys	Glu
				710					715					720
Thr	Leu	Arg	Pro	Gly	Glu	Lys	Ala	Pro	Leu	Ser	Arg	Glu	Gln	His
				725					730					735
Leu	Gln	Ser	Pro	Lys	Glu	Cys	Arg	Thr	Ser	Ala	Ser	Asp	Val	Asp
				740					745					750
Ala	Asp	Asn	Asn	Cys	Leu	Gly	Thr	Glu	Val	Ala				
				755					760					

<210> 278  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 278  
 ctgctggtga aatctggcgt ggag 24

<210> 279  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 279  
gtctggtcct ggctgtccac ccag 24

<210> 280  
<211> 45  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 280  
catcttgta tgtacctggg aaccaccaca gggtcgctcc acaag 45

<210> 281  
<211> 2320  
<212> DNA  
<213> Homo sapiens

<400> 281  
agggtccctt agccgggcgc agggcgcgca gccaggctg agatccgcgg 50  
cttccgtaga agtgagcatg gctgggcagc gagtgttct tctagtgggc 100  
ttccttctcc ctggggtcct gctctcagag gctgccaaaa tctgacaat 150  
atctacagta ggtggaagcc attatctact gatggaccgg gtttctcaga 200  
ttcttcaaga tcacggtcat aatgtcacca tgcttaacca caaaagaggt 250  
ccttttatgc cagattttaa aaaggaagaa aaatcatatc aagttatcag 300  
ttggcttgca cctgaagatc atcaaagaga atttaaaaag agttttgatt 350  
tctttctgga agaaacttta ggtggcagag gaaaatttga aaacttatta 400  
aatgttctag aatacttggc gttgcagtgc agtcattttt taaatagaaa 450  
ggatatcatg gattccttaa agaagagaaa ctacgacatg gtgatagttg 500  
aaacttttga ctactgtcct ttcttgattg ctgagaagct tgggaagcca 550  
tttgtggcca ttctttccac ttcatcggc tctttggaat ttgggctacc 600  
aatccccttg tcttatgttc cagtattccg ttcttgctg actgatcaca 650  
tggacttctg gggccgagtg aagaattttc tgatgttctt tagtttctgc 700  
aggaggcaac agcacatgca gtctacattt gacaacacca tcaaggaaca 750  
tttcacagaa ggctctaggc cagttttgtc tcatcttcta ctgaaagcag 800  
agttgtggtt cattaactct gactttgcct ttgattttgc tcgacctctg 850  
cttcccaaca ctgtttatgt tggaggcttg atggaaaaac ctattaaacc 900

agtaccacaa gacttggaga acttcattgc caagtttggg gactctgggt 950  
 ttgtccttgt gaccttgggc tccatggtga acacctgtca gaatccggaa 1000  
 atcttcaagg agatgaacaa tgcctttgct cacctacccc aaggggtgat 1050  
 atggaagtgt cagtgttctc attggcccaa agatgtccac ctggctgcaa 1100  
 atgtgaaaat tgtggactgg ctctctcaga gtgacctcct ggctcaccga 1150  
 agcatccgtc tgtttgtcac ccacggcggg cagaatagca taatggaggc 1200  
 catccagcat ggtgtgcca tgggtgggat ccctctcttt ggagaccagc 1250  
 ctgaaaacat ggtccgagta gaagccaaaa agtttgggtg ttctattcag 1300  
 ttaaagaagc tcaaggcaga gacattggct cttaatga aacaaatcat 1350  
 ggaagacaag agatacaagt ccgcggcagt ggctgccagt gtcctcctgc 1400  
 gctcccaccc gctcagcccc acacagcggc tgggtgggctg gattgaccac 1450  
 gtctccaga cagggggcgc gacgcacctc aagccctatg tctttcagca 1500  
 gccctggcat gagcagtacc tgttcgacgt ttttgtgttt ctgctggggc 1550  
 tcaactctggg gactctatgg ctttgtggga agctgctggg catggctgtc 1600  
 tgggtggctgc gtggggccag aaagggtgaag gagacataag gccagggtgca 1650  
 gccttgggcg ggtctgtttg gtgggcgatg tcaccatttc tagggagctt 1700  
 cccactagtt ctggcagccc cattctctag tccttctagt tatctcctgt 1750  
 tttcttgaag aacaggaaaa atggccaaaa atcatccttt ccacttgcta 1800  
 attttgctac aaattcatcc ttactagctc ctgcctgcta gcagaaatct 1850  
 ttccagtcct cttgtcctcc tttgtttgcc atcagcaagg gctatgctgt 1900  
 gattctgtct ctgagtgact tggaccactg accctcagat ttccagcctt 1950  
 aaaatccacc ttctttctca tgcgcctctc cgaatcacac cctgactctt 2000  
 ccagcctcca tgtccagacc tagtcagcct ctctcactcc tgcccctact 2050  
 atctatcatg gaataacatc caagaaagac accttgcata ttctttcagt 2100  
 ttctgttttg ttctcccaca tattctcttc aatgctcagg aagcctgccc 2150  
 tgtgcttgag agttcagggc cggacacagg ctacaggtc tccacattgg 2200  
 gtccctgtct ctggtgcca cagtgaagctc cttcttggct gagcaggcat 2250  
 ggagactgta ggtttccaga tttcctgaaa aataaaagt ttacagcgta 2300  
 tctctcccca acctcactaa 2320

<210> 282  
 <211> 523  
 <212> PRT  
 <213> Homo sapiens

<400> 282

Met	Ala	Gly	Gln	Arg	Val	Leu	Leu	Leu	Val	Gly	Phe	Leu	Leu	Pro
1				5					10					15
Gly	Val	Leu	Leu	Ser	Glu	Ala	Ala	Lys	Ile	Leu	Thr	Ile	Ser	Thr
				20					25					30
Val	Gly	Gly	Ser	His	Tyr	Leu	Leu	Met	Asp	Arg	Val	Ser	Gln	Ile
				35					40					45
Leu	Gln	Asp	His	Gly	His	Asn	Val	Thr	Met	Leu	Asn	His	Lys	Arg
				50					55					60
Gly	Pro	Phe	Met	Pro	Asp	Phe	Lys	Lys	Glu	Glu	Lys	Ser	Tyr	Gln
				65					70					75
Val	Ile	Ser	Trp	Leu	Ala	Pro	Glu	Asp	His	Gln	Arg	Glu	Phe	Lys
				80					85					90
Lys	Ser	Phe	Asp	Phe	Phe	Leu	Glu	Glu	Thr	Leu	Gly	Gly	Arg	Gly
				95					100					105
Lys	Phe	Glu	Asn	Leu	Leu	Asn	Val	Leu	Glu	Tyr	Leu	Ala	Leu	Gln
				110					115					120
Cys	Ser	His	Phe	Leu	Asn	Arg	Lys	Asp	Ile	Met	Asp	Ser	Leu	Lys
				125					130					135
Asn	Glu	Asn	Phe	Asp	Met	Val	Ile	Val	Glu	Thr	Phe	Asp	Tyr	Cys
				140					145					150
Pro	Phe	Leu	Ile	Ala	Glu	Lys	Leu	Gly	Lys	Pro	Phe	Val	Ala	Ile
				155					160					165
Leu	Ser	Thr	Ser	Phe	Gly	Ser	Leu	Glu	Phe	Gly	Leu	Pro	Ile	Pro
				170					175					180
Leu	Ser	Tyr	Val	Pro	Val	Phe	Arg	Ser	Leu	Leu	Thr	Asp	His	Met
				185					190					195
Asp	Phe	Trp	Gly	Arg	Val	Lys	Asn	Phe	Leu	Met	Phe	Phe	Ser	Phe
				200					205					210
Cys	Arg	Arg	Gln	Gln	His	Met	Gln	Ser	Thr	Phe	Asp	Asn	Thr	Ile
				215					220					225
Lys	Glu	His	Phe	Thr	Glu	Gly	Ser	Arg	Pro	Val	Leu	Ser	His	Leu
				230					235					240
Leu	Leu	Lys	Ala	Glu	Leu	Trp	Phe	Ile	Asn	Ser	Asp	Phe	Ala	Phe
				245					250					255
Asp	Phe	Ala	Arg	Pro	Leu	Leu	Pro	Asn	Thr	Val	Tyr	Val	Gly	Gly



260	265	270
Leu Met Glu Lys Pro Ile Lys Pro Val	Pro Gln Asp Leu Glu Asn	
275	280	285
Phe Ile Ala Lys Phe Gly Asp Ser Gly	Phe Val Leu Val Thr Leu	
290	295	300
Gly Ser Met Val Asn Thr Cys Gln Asn	Pro Glu Ile Phe Lys Glu	
305	310	315
Met Asn Asn Ala Phe Ala His Leu Pro	Gln Gly Val Ile Trp Lys	
320	325	330
Cys Gln Cys Ser His Trp Pro Lys Asp	Val His Leu Ala Ala Asn	
335	340	345
Val Lys Ile Val Asp Trp Leu Pro Gln	Ser Asp Leu Leu Ala His	
350	355	360
Pro Ser Ile Arg Leu Phe Val Thr His	Gly Gly Gln Asn Ser Ile	
365	370	375
Met Glu Ala Ile Gln His Gly Val Pro	Met Val Gly Ile Pro Leu	
380	385	390
Phe Gly Asp Gln Pro Glu Asn Met Val	Arg Val Glu Ala Lys Lys	
395	400	405
Phe Gly Val Ser Ile Gln Leu Lys Lys	Leu Lys Ala Glu Thr Leu	
410	415	420
Ala Leu Lys Met Lys Gln Ile Met Glu	Asp Lys Arg Tyr Lys Ser	
425	430	435
Ala Ala Val Ala Ala Ser Val Ile Leu	Arg Ser His Pro Leu Ser	
440	445	450
Pro Thr Gln Arg Leu Val Gly Trp Ile	Asp His Val Leu Gln Thr	
455	460	465
Gly Gly Ala Thr His Leu Lys Pro Tyr	Val Phe Gln Gln Pro Trp	
470	475	480
His Glu Gln Tyr Leu Phe Asp Val Phe	Val Phe Leu Leu Gly Leu	
485	490	495
Thr Leu Gly Thr Leu Trp Leu Cys Gly	Lys Leu Leu Gly Met Ala	
500	505	510
Val Trp Trp Leu Arg Gly Ala Arg Lys	Val Lys Glu Thr	
515	520	

<210> 283  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 283  
 tgcctttgct cacctacccc aagg 24

<210> 284  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 284  
 tcaggctggt ctccaaagag aggg 24

<210> 285  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 285  
 cccaaagatg tccacctggc tgcaaattgtg aaaattgtgg actgg 45

<210> 286  
 <211> 2340  
 <212> DNA  
 <213> Homo sapiens

<400> 286  
 gggctgttga tttgtggggg attttgaaga gaggaggaat aggaggaagg 50  
 ggttgagggg ctgcctcttg catatgcaca cactcacaca ttctgtcaca 100  
 cccgtcacac acacatacca tgttctccat cccccagggt ccagccctca 150  
 gtgctgtccc atccagcagg gctacctga agctctggct gcagccctcc 200  
 cgtccagtgg gcaggcggct tcatccctcc tttctctccc aaagcccaac 250  
 tgctgtcact gcatgctctg ccaaggagga gggaactgca gtgacagcag 300  
 gagtaagagt gggaggcagg acagagctgg gacacaggta tggagagggg 350  
 gttcagcgag cctagagagg gcagactatc aggggtgccg cggtgagaat 400  
 ccagggagag gagcggaac agaagagggg cagaagaccg gggcacttgt 450

gggttgcaga gccctcagc catgttggga gccaaagccac actggctacc 500  
 aggtccccta cacagtcccg ggctgccctt ggttctgggtg cttctggccc 550  
 tgggggccgg gtgggccag gaggggtcag agcccgctct gctggagggg 600  
 gagtgcctgg tggctctgtga gcctggccga gctgctgcag gggggcccgg 650  
 gggagcagcc ctgggagagg cccccctgg gcgagtggca tttgctgcgg 700  
 tccgaagcca ccacatgag ccagcagggg aaaccggcaa tggcaccagt 750  
 ggggccatct acttcgacca ggtcctgggtg aacgagggcg gtggctttga 800  
 ccgggcctct ggctccttcg tagccctgt ccggggtgtc tacagcttcc 850  
 ggttccatgt ggtgaagggtg tacaaccgcc aaactgtcca ggtgagcctg 900  
 atgctgaaca cgtggcctgt catctcagcc tttgccaatg atcctgacgt 950  
 gaccggggag gcagccacca gctctgtgct actgcccttg gaccctgggg 1000  
 accgagtgtc tctgcgcctg cgtcggggga atctactggg tggttggaaa 1050  
 tactcaagtt tctctggctt cctcatcttc cctctctgag gacccaagtc 1100  
 tttcaagcac aagaatccag cccctgacaa ctttcttctg ccctctcttg 1150  
 cccagaaac agcagaggca ggagagagac tccctctggc tcctatccca 1200  
 cctctttgca tgggaccctg tgccaaacac ccaagtttaa gagaagagta 1250  
 gagctgtggc atctccagac caggcctttc caccaccca ccccagtta 1300  
 ccctcccagc cacctgctgc atctgttctt gcctgcagcc ctaggatcag 1350  
 ggcaaggttt ggcaagaagg aagatctgca ctactttgcg gcctctgctc 1400  
 ctccggttcc cccaccccag cttcctgctc aatgctgatc agggacaggt 1450  
 ggcgcagggtg agcctgacag gccccacag gagccagat ggacaagcct 1500  
 cagcgtaccc tgcaggcttc ttctgtgag gaaagccagc atcacggatc 1550  
 tcagccagca ccgtcagaag ctgagccagc accgtatggg ctagggtggg 1600  
 aggctcagcc acaggcagaa ggggtgggaag ggcctggagt ctgtggctgg 1650  
 tgaggaagga aggaggggtgt attgtctaga ctgaacatgg tacacattct 1700  
 gcatgtatag cagagcagcc agcaggtagc aatcctggct gtccttctat 1750  
 gctggatccc agatggactc tggcccttac ctccccacct gagattaggg 1800  
 tgagtgtgtt tgctctggct gagagcagag ctgagagcag gtatacagag 1850  
 ctggaagtgg accatggaaa acatcgataa ccatgcatcc tcttgcttgg 1900

ccacctcctg aaactgctcc acctttgaag tttgaacttt agtccctcca 1950  
 cactctgaact gctgctcct tctcccagc tctctcactg agttatcttc 2000  
 actgtacctg ttccagcata tccccactat ctctctttct cctgatctgt 2050  
 gctgtcttat tctcctcctt aggcttecta ttacctggga ttccatgatt 2100  
 cattccttca gaccctctcc tgccagtatg ctaaaccctc cctctctctt 2150  
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 caactagaga atggtggtca gtgagacact atagaattac taaggagaag 2250  
 atgcctctgg agtttggatc ggggtgttaca ggtacaagta ggtatgttgc 2300  
 agaggaaaat aaatatcaaa ctgtatacta aaattaaaaa 2340

<210> 287  
 <211> 205  
 <212> PRT  
 <213> Homo sapiens

<400> 287  
 Met Leu Gly Ala Lys Pro His Trp Leu Pro Gly Pro Leu His Ser  
 1 5 10 15  
 Pro Gly Leu Pro Leu Val Leu Val Leu Leu Ala Leu Gly Ala Gly  
 20 25 30  
 Trp Ala Gln Glu Gly Ser Glu Pro Val Leu Leu Glu Gly Glu Cys  
 35 40 45  
 Leu Val Val Cys Glu Pro Gly Arg Ala Ala Ala Gly Gly Pro Gly  
 50 55 60  
 Gly Ala Ala Leu Gly Glu Ala Pro Pro Gly Arg Val Ala Phe Ala  
 65 70 75  
 Ala Val Arg Ser His His His Glu Pro Ala Gly Glu Thr Gly Asn  
 80 85 90  
 Gly Thr Ser Gly Ala Ile Tyr Phe Asp Gln Val Leu Val Asn Glu  
 95 100 105  
 Gly Gly Gly Phe Asp Arg Ala Ser Gly Ser Phe Val Ala Pro Val  
 110 115 120  
 Arg Gly Val Tyr Ser Phe Arg Phe His Val Val Lys Val Tyr Asn  
 125 130 135  
 Arg Gln Thr Val Gln Val Ser Leu Met Leu Asn Thr Trp Pro Val  
 140 145 150  
 Ile Ser Ala Phe Ala Asn Asp Pro Asp Val Thr Arg Glu Ala Ala  
 155 160 165  
 Thr Ser Ser Val Leu Leu Pro Leu Asp Pro Gly Asp Arg Val Ser

	170		175		180
Leu Arg Leu Arg Arg Gly Asn Leu Leu Gly Gly Trp Lys Tyr Ser					
	185		190		195
Ser Phe Ser Gly Phe Leu Ile Phe Pro Leu					
	200		205		

<210> 288  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 288  
 aggcagccac cagctctgtg ctac 24

<210> 289  
 <211> 27  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-27  
 <223> Synthetic construct.

<400> 289  
 cagagaggga agatgaggaa gccagag 27

<210> 290  
 <211> 42  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-42  
 <223> Synthetic construct.

<400> 290  
 ctgtgctact gcccttgac cctggggacc gagtgtctct gc 42

<210> 291  
 <211> 1570  
 <212> DNA  
 <213> Homo sapiens

<400> 291  
 gctgtttctc tcgcgccacc actggccgcc ggccgcagct ccaggtgtcc 50  
 tagccgccca gcctcgacgc cgtoceggga ccctgtgtct ctgcgcgaag 100  
 ccctggcccc gggggccggg gcatgggcca ggggcgcggg gtgaagcggc 150



<210> 292  
 <211> 388  
 <212> PRT  
 <213> Homo sapiens

<400> 292

Met	Lys	Thr	Leu	Ile	Ala	Ala	Tyr	Ser	Gly	Val	Leu	Arg	Gly	Glu
1				5					10					15
Arg	Gln	Ala	Glu	Ala	Asp	Arg	Ser	Gln	Arg	Ser	His	Gly	Gly	Pro
				20					25					30
Ala	Leu	Ser	Arg	Glu	Gly	Ser	Gly	Arg	Trp	Gly	Thr	Gly	Ser	Ser
				35					40					45
Ile	Leu	Ser	Ala	Leu	Gln	Asp	Leu	Phe	Ser	Val	Thr	Trp	Leu	Asn
				50					55					60
Arg	Ser	Lys	Val	Glu	Lys	Gln	Leu	Gln	Val	Ile	Ser	Val	Leu	Gln
				65					70					75
Trp	Val	Leu	Ser	Phe	Leu	Val	Leu	Gly	Val	Ala	Cys	Ser	Ala	Ile
				80					85					90
Leu	Met	Tyr	Ile	Phe	Cys	Thr	Asp	Cys	Trp	Leu	Ile	Ala	Val	Leu
				95					100					105
Tyr	Phe	Thr	Trp	Leu	Val	Phe	Asp	Trp	Asn	Thr	Pro	Lys	Lys	Gly
				110					115					120
Gly	Arg	Arg	Ser	Gln	Trp	Val	Arg	Asn	Trp	Ala	Val	Trp	Arg	Tyr
				125					130					135
Phe	Arg	Asp	Tyr	Phe	Pro	Ile	Gln	Leu	Val	Lys	Thr	His	Asn	Leu
				140					145					150
Leu	Thr	Thr	Arg	Asn	Tyr	Ile	Phe	Gly	Tyr	His	Pro	His	Gly	Ile
				155					160					165
Met	Gly	Leu	Gly	Ala	Phe	Cys	Asn	Phe	Ser	Thr	Glu	Ala	Thr	Glu
				170					175					180
Val	Ser	Lys	Lys	Phe	Pro	Gly	Ile	Arg	Pro	Tyr	Leu	Ala	Thr	Leu
				185					190					195
Ala	Gly	Asn	Phe	Arg	Met	Pro	Val	Leu	Arg	Glu	Tyr	Leu	Met	Ser
				200					205					210
Gly	Gly	Ile	Cys	Pro	Val	Ser	Arg	Asp	Thr	Ile	Asp	Tyr	Leu	Leu
				215					220					225
Ser	Lys	Asn	Gly	Ser	Gly	Asn	Ala	Ile	Ile	Ile	Val	Val	Gly	Gly
				230					235					240
Ala	Ala	Glu	Ser	Leu	Ser	Ser	Met	Pro	Gly	Lys	Asn	Ala	Val	Thr
				245					250					255
Leu	Arg	Asn	Arg	Lys	Gly	Phe	Val	Lys	Leu	Ala	Leu	Arg	His	Gly

260	265	270
Ala Asp Leu Val Pro Ile Tyr Ser Phe Gly Glu Asn Glu Val Tyr		
275	280	285
Lys Gln Val Ile Phe Glu Glu Gly Ser Trp Gly Arg Trp Val Gln		
290	295	300
Lys Lys Phe Gln Lys Tyr Ile Gly Phe Ala Pro Cys Ile Phe His		
305	310	315
Gly Arg Gly Leu Phe Ser Ser Asp Thr Trp Gly Leu Val Pro Tyr		
320	325	330
Ser Lys Pro Ile Thr Thr Val Val Gly Glu Pro Ile Thr Ile Pro		
335	340	345
Lys Leu Glu His Pro Thr Gln Gln Asp Ile Asp Leu Tyr His Thr		
350	355	360
Met Tyr Met Glu Ala Leu Val Lys Leu Phe Asp Lys His Lys Thr		
365	370	375
Lys Phe Gly Leu Pro Glu Thr Glu Val Leu Glu Val Asn		
380	385	

<210> 293  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 293  
 gctgacctgg ttcccatcta ctcc 24

<210> 294  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 294  
 cccacagaca cccatgacac ttcc 24

<210> 295  
 <211> 50  
 <212> DNA  
 <213> Artificial

<220>



<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 295  
aagaatgaat tgtacaaagc aggtgatctt cgaggagggc tcctggggcc 50

<210> 296  
<211> 3060  
<212> DNA  
<213> Homo sapiens

<400> 296  
gggcggcgagg atggggggccg gggggcgccg gcgccgact cgctgaggcc 50  
ccgacgcagg gccggggccg gccaggggc gaggagcgc gcggccagag 100  
cggggcccgc gagggcgacgc cggggacgcc cgcgcgacga gcaggtggcg 150  
gcggctgcag gcttgtccag ccggaagccc tgagggcagc tgttcccact 200  
ggctctgctg accttgtgcc ttggacggct gtcctcagcg aggggccgtg 250  
caccgcctcc tgagcagcgc catgggcctg ctggccttcc tgaagacca 300  
gttcgtgctg caoctgctgg tcggctttgt cttcgtggcg agtggctctg 350  
tcatcaactt cgtccagctg tgcacgctgg cgctctggcc ggtcagcaag 400  
cagctctacc gccgcctcaa ctgccgcctc gcctactcac tctggagcca 450  
actggcatg ctgctggagt ggtggctctg cacggagtgt aactgttca 500  
cggaccaggc cacggtagag cgctttggga aggagcacgc agtcatcatc 550  
ctcaaccaca acttcgagat cgacttcctc tgtgggtgga ccatgtgtga 600  
gcgcttcgga gtgctgggga gctccaaggc cctcgctaag aaggagctgc 650  
tctacgtgcc cctcatggc tggacgtggc actttctgga gattgtgttc 700  
tgcaagcgga agtgggagga ggaccgggac accgtggctg aagggtctag 750  
gcgcctgtcg gactaccccg agtacatgtg gtttctcctg tactgcgagg 800  
ggacgcgctt cacggagacc aagcaaccgc ttagcatgga ggtggcggtc 850  
gctaaggggc ttctgtcct caagtaccac ctgctgccgc ggaccaaggg 900  
cttcaccacc gcagtcaagt gcctccgggg gacagtcgca gctgtctatg 950  
atgtaaccct gaacttcaga ggaaacaaga acccgctcct gctggggatc 1000  
ctctacggga agaagtacga ggccgacatg tgcgtgagga gatttcctct 1050  
ggaagacatc ccgctggatg aaaaggaagc agctcagtg cttcataaac 1100  
tgtaccagga gaaggacgcg ctccaggaga tatataatca gaaggcatg 1150

tttccagggg agcagtttaa gcctgcccgg aggccgtgga ccctcctgaa 1200  
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 tggggtcttt tgccagcgga tcacctctcc tgatcctgac tttcttgggg 1300  
 tttgtgggag cagcttcctt tggagtctgc agactgatag gagaatcgct 1350  
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 ccagcctagg caacagagca agactcagtc tcaaaaaaaaa aaaaaaaca 1450  
 aaaaacccca gaaattcttg agttgaactg tgtagttact gacatgaaaa 1500  
 attcactaga ggctgaacag cagatttgag caggcagaaa aaaatcagca 1550  
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 aggaaaatta acagcctcag agacctatgg tgcaccgtca cacaaatcaa 1650  
 catatgcatg atgagagtcc cagaaggaga ggagagaaaag ggtcagaaaag 1700  
 aatggccaca agctgatgaa aaacagtaac ctaccactc aggaagctca 1750  
 gtgaactcca atgaggatga atatcagaga tccacaccta gatatttcat 1800  
 aatcaaagtg tcaaatagca aagaatcttg aaagcagcaa gagatgagca 1850  
 acttatcttg ttcaaaggat ctttgatcag attaacagct catttctcct 1900  
 cagaaatcat gggagccagg agatagtggg atgaacactg ttgaaggcaa 1950  
 aaccttcaac tgtaattatt ggacttttga gtcttagatg gtcctgacct 2000  
 ctttgtcttc agggacagtt tttcaattta atccctaata acaattagtc 2050  
 aagcttcctt gacctgtagg aaggcctgtc tttaggccgg gcacagtggc 2100  
 ttacacctgt aatcccagca ctttgggagg ccagacggg tggatcattt 2150  
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 gtgatcccaa gtagcttga ttgtaaacad gcaccacat gcctggctaa 2350  
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 gacctcaagt gaccacctgc ctacgcctcc caaagtactg ggattacagg 2450  
 cgtgagccac tgtgcctggc cttgagcatc ttgtgatgtg cttattggcc 2500  
 atttgtatat cttctatctt ctttggggaa atgtctgttc aagtcctttg 2550  
 cctttttaaa tttttattat ttatttattt atttattttg agacagggtc 2600

ttgttctggt gcccaggctg gactacagtgc gcacagtctt ggctcactgc 2650  
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 agctgtattt tttgtattt tgtattttgt agctgtagtt tttgtattt 2750  
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 catgagccac tgcacctggc aaactcccaa aattcaacac acacacacaa 2900  
 aaaaccacct gattcaaat gggcagaggg gccgggtgtg gcccacta 2950  
 ccaggagac tgaagtggga ggatcgcttg ggcagagaa gtcgaggctg 3000  
 cagtgagtcg aggttgtgcg actgcattcc agcctggaca acagagtgcg 3050  
 accctgtctc 3060

<210> 297  
 <211> 368  
 <212> PRT  
 <213> Homo sapiens

<400> 297  
 Met Gly Leu Leu Ala Phe Leu Lys Thr Gln Phe Val Leu His Leu  
 1 5 10 15  
 Leu Val Gly Phe Val Phe Val Val Ser Gly Leu Val Ile Asn Phe  
 20 25 30  
 Val Gln Leu Cys Thr Leu Ala Leu Trp Pro Val Ser Lys Gln Leu  
 35 40 45  
 Tyr Arg Arg Leu Asn Cys Arg Leu Ala Tyr Ser Leu Trp Ser Gln  
 50 55 60  
 Leu Val Met Leu Leu Glu Trp Trp Ser Cys Thr Glu Cys Thr Leu  
 65 70 75  
 Phe Thr Asp Gln Ala Thr Val Glu Arg Phe Gly Lys Glu His Ala  
 80 85 90  
 Val Ile Ile Leu Asn His Asn Phe Glu Ile Asp Phe Leu Cys Gly  
 95 100 105  
 Trp Thr Met Cys Glu Arg Phe Gly Val Leu Gly Ser Ser Lys Val  
 110 115 120  
 Leu Ala Lys Lys Glu Leu Leu Tyr Val Pro Leu Ile Gly Trp Thr  
 125 130 135  
 Trp Tyr Phe Leu Glu Ile Val Phe Cys Lys Arg Lys Trp Glu Glu  
 140 145 150  
 Asp Arg Asp Thr Val Val Glu Gly Leu Arg Arg Leu Ser Asp Tyr  
 155 160 165



<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-21

<223> Synthetic construct.

<400> 299

gccacctcca tgctaacgcg g 21

<210> 300

<211> 45

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-45

<223> Synthetic construct.

<400> 300

ccaaggtcct cgctaagaag gagctgctct acgtgccct catcg 45

<210> 301

<211> 1334

<212> DNA

<213> Homo sapiens

<400> 301

gatattcttt atttttaaga atctgaagta ctatgcatca ctccctccaa 50  
 tgtcctgggg cagccaccag gcatattcat ctttgtgtgt gtttttcttt 100  
 tgcttttagca ctggggcact tcttgcttat ttctttggta ggaaaggggc 150  
 tcagtttgtc ttgtgggggt ggtggcaggc aggccggctt acgcctgata 200  
 cgcccttggg ttagaaggga agggaagata aacttttata caaatgggga 250  
 tagctgggggt ctgagacctg ctctctcagt aaaattcctg ggatctgcct 300  
 ataccttctt ttctctaacc tggcataccc tgcttaaagc ctctcagggc 350  
 ttctctctgt tcttaggatc aaagtattta gagctacaag agccctcatg 400  
 gtctggcccc tgccccctg gccagcttca ttgtacatgt ggtgttctct 450  
 tgtcgttcct gtaatgtggt atgccatggg gtctttgcac aagcctttcc 500  
 tctttggctg gacactgttc cctgcccccc ccatactctt cctacttaat 550  
 atgtagtcat cctgcagatt tcaattctaa catcattttc tccagggatc 600  
 ctggcctgac agaatctcat cttgtttaat gctctcataa gaccacttgt 650  
 ttcccttttg cagcacttgc cactcagttg tatctttatg tgcgtttgtg 700  
 gttgtatggg ttgtgtctgt tccccagaat gccagctct gagctgcgtg 750

agggtcaagg gcattgctgt gcctgccagg tatagtgcct acatgtggtg 800  
 ggtgctcatg ttttagagac taaatggagg aggagatgag gaaaagattg 850  
 aaatctctca gttcaccaga tgggtgtaggg ccagcattg taaattcaca 900  
 cgttgactgt gcttgtgaat tatctgggga tgcaggtcct gattcagtag 950  
 gccaggttg ggcattctcta acaaaactccc acgtgatgct gatgctggtc 1000  
 ctatgaacta tactaaatag taagaatcta tggagccagg ctgggcatgg 1050  
 tggctcacac ctatgatccc agcactttgg gaggtgagg caggctgata 1100  
 acctggagtc aggatttcaa gactagcctg gccaacatgg tggaacccca 1150  
 tctgtactaa aaatacacia attagctggg catggtggca catgcctgta 1200  
 gtcccagcta cttgggaggc tgaagcaaga gaatcgcttg aacctgggag 1250  
 gcggagggtg cagtgaagcc agatcaggcc actgtattcc aaccagggtg 1300  
 acagagtga actctatgtc caaaaaaaaa aaaa 1334

<210> 302  
 <211> 143  
 <212> PRT  
 <213> Homo sapiens

<400> 302  
 Met His His Ser Leu Gln Cys Pro Gly Ala Ala Thr Arg His Ile  
 1 5 10 15  
 His Leu Cys Val Cys Phe Ser Phe Ala Leu Ala Leu Gly His Phe  
 20 25 30  
 Leu Leu Ile Ser Leu Val Gly Lys Gly Leu Ser Leu Ser Cys Gly  
 35 40 45  
 Val Gly Gly Arg Gln Ala Gly Leu Arg Leu Ile Arg Pro Trp Val  
 50 55 60  
 Arg Arg Glu Gly Lys Ile Asn Phe Tyr Thr Asn Gly Asp Ser Trp  
 65 70 75  
 Gly Leu Arg Pro Ala Ser Ser Val Lys Phe Leu Gly Ser Ala Tyr  
 80 85 90  
 Thr Phe Phe Ser Leu Thr Trp His Thr Leu Leu Lys Ala Ser Gln  
 95 100 105  
 Gly Phe Ser Leu Phe Leu Gly Ser Lys Tyr Leu Glu Leu Gln Glu  
 110 115 120  
 Pro Ser Trp Ser Gly Pro Cys Pro Pro Gly Gln Leu His Cys Thr  
 125 130 135  
 Cys Gly Val Leu Leu Ser Phe Leu

<210> 303  
 <211> 1768  
 <212> DNA  
 <213> Homo sapiens

<400> 303  
 ggctggactg gaactcctgg tcccaagtga tccacccgcc tcagcctccc 50  
 aagggtgctgt gattataggt gtaagccacc gtgtctggcc tctgaacaac 100  
 tttttcagca actaaaaaag ccacaggagt tgaactgcta ggattctgac 150  
 tatgctgtgg tggctagtgc tcctactcct acctacatta aaatctgttt 200  
 tttgttctct tgtaactagc ctttaccttc ctaacacaga ggatctgtca 250  
 ctgtggctct ggcccaaacc tgaccttcac tctggaacga gaacagaggt 300  
 ttctaccac accgtcccct cgaagccggg gacagcctca ccttgctggc 350  
 ctctcgctgg agcagtggc tcaccaactg tctcacgtct ggaggcactg 400  
 actcgggcag tgcaggtagc tgagcctctt ggtagctgcg gctttcaagg 450  
 tgggccttgc cctggccgta gaagggattg acaagcccga agatttcata 500  
 ggcgatggct cccactggcc aggcatcagc cttgctgtag tcaatcactg 550  
 ccctggggcc aggaaggcc gtggacacct gctcagaagc agtgggtgag 600  
 acatcacgtc gcccgcccat ctaacctttt catgtcctgc acatcacctg 650  
 atccatgggc taatctgaac tctgtcccaa ggaaccaga gcttgagtga 700  
 gctgtggctc agaccagaa ggggtctgct tagaccacct ggtttatgtg 750  
 acaggacttg cattctcctg gaacatgagg gaacgccgga ggaaagcaaa 800  
 gtggcaggga aggaacttgt gccaaattat gggtcagaaa agatggaggt 850  
 gttgggttat cacaaggcat cgagtctcct gcattcagtg gacatgtggg 900  
 ggaagggtc cccgatggcg atgacacact cgggactcac ctctggggcc 950  
 atcagacagc cgtttccgcc ccgatccagc taccagctgc tgaagggcaa 1000  
 ctgcaggccg atgctctcat cagccaggca gcagccaaaa tctgcgatca 1050  
 ccagccaggg gcagccgtct gggaaggagc aagcaaagt accatttctc 1100  
 ctccccctc tccctctgag aggccctcct atgtccctac taaagccacc 1150  
 agcaagacat agctgacagg ggctaattgg tcagtgttgg cccaggaggt 1200  
 cagcaaggcc tgagagctga tcagaagggc ctgctgtgcg aacacggaaa 1250

tgccctccagt aagcacaggc tgcaaaatcc ccaggcaaag gactgtgtgg 1300  
 ctcaatttaa atcatgttct agtaattgga gctgtcccca agaccaaag 1350  
 agctagagct tgggttcaat gatctccaag ggcccttata cccaggaga 1400  
 ctttgatttg aatttgaaac cccaaatcca aacctagaa ccagggtgcat 1450  
 taagaatcag ttattgccgg gtgtggtggc ctgtaatgcc aacattttgg 1500  
 gaggccgagg cgggtagatc acctgaggtc aggagttcaa gaccagcctg 1550  
 gccaacatgg tgaaaccctt gtctctacta aaaatacaaa aaaactagcc 1600  
 aggcattgtg gtgtgtgcct gtatcccagc tactcgggag gctgagacag 1650  
 gagaattact tgaacctggg aggtgaagga ggctgagaca ggagaatcac 1700  
 ttcagcctga gcaacacagc gagactctgt ctcagaaaaa ataaaaaaag 1750  
 aattatggtt atttgtaa 1768

<210> 304  
 <211> 109  
 <212> PRT  
 <213> Homo sapiens

<400> 304  
 Met Leu Trp Trp Leu Val Leu Leu Leu Leu Pro Thr Leu Lys Ser  
 1 5 10 15  
 Val Phe Cys Ser Leu Val Thr Ser Leu Tyr Leu Pro Asn Thr Glu  
 20 25 30  
 Asp Leu Ser Leu Trp Leu Trp Pro Lys Pro Asp Leu His Ser Gly  
 35 40 45  
 Thr Arg Thr Glu Val Ser Thr His Thr Val Pro Ser Lys Pro Gly  
 50 55 60  
 Thr Ala Ser Pro Cys Trp Pro Leu Ala Gly Ala Val Pro Ser Pro  
 65 70 75  
 Thr Val Ser Arg Leu Glu Ala Leu Thr Arg Ala Val Gln Val Ala  
 80 85 90  
 Glu Pro Leu Gly Ser Cys Gly Phe Gln Gly Gly Pro Cys Pro Gly  
 95 100 105  
 Arg Arg Arg Asp

<210> 305  
 <211> 989  
 <212> DNA  
 <213> Homo sapiens

<400> 305



gcgggcccgc gagtccgaga cctgtcccag gagctccagc tcacgtgacc 50  
 tgtaactgcc tcccgcgcgc tctgtcccgc gccatgaccc agccggtgcc 100  
 ccggtctctcc gtgcccgcgc cgctggccct gggctcagcc gcactgggcg 150  
 ccgccttcgc cactggcctc ttcctgggga ggcggtgcc cccatggcga 200  
 ggccggcgag agcagtgcct gcttcccccc gaggacagcc gcctgtggca 250  
 gtatcttctg agccgctcca tgcgggagca ccgggcgctg cgaagcctga 300  
 ggctgctgac cctggagcag ccgcagggggg attctatgat gacctgcgag 350  
 caggcccagc tcttggccaa cctggcgcgg ctcatccagg ccaagaaggc 400  
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 cgctgcccgc ggacgggcg gcgtgtgacct gcgaggtgga cgcgagccc 500  
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 aactgctccg cctactacga gcgtgcctg cagctgctgc gaccgaggag 700  
 catcctcgcc gtcctcagag tctgtggcg cggaagggtg ctgcaacctc 750  
 cgaaagggga cgtggcggcc gagtgtgtgc gaaacctaaa cgaacgcac 800  
 cggcgggacg tcagggtcta catcagcctc ctgcccctgg gcgatggact 850  
 caccttggcc ttcaagatct agggctggcc cctagtgagt gggctcgagg 900  
 gagggttgcc tgggaacccc aggaattgac cctgagtttt aaattcgaaa 950  
 ataaagtggg gctgggacac aaaaaaaaaa aaaaaaaaaa 989

<210> 306  
 <211> 262  
 <212> PRT  
 <213> Homo sapiens

<400> 306  
 Met Thr Gln Pro Val Pro Arg Leu Ser Val Pro Ala Ala Leu Ala  
 1 5 10 15  
 Leu Gly Ser Ala Ala Leu Gly Ala Ala Phe Ala Thr Gly Leu Phe  
 20 25 30  
 Leu Gly Arg Arg Cys Pro Pro Trp Arg Gly Arg Arg Glu Gln Cys  
 35 40 45  
 Leu Leu Pro Pro Glu Asp Ser Arg Leu Trp Gln Tyr Leu Leu Ser  
 50 55 60

Arg	Ser	Met	Arg	Glu	His	Pro	Ala	Leu	Arg	Ser	Leu	Arg	Leu	Leu	65	70	75
Thr	Leu	Glu	Gln	Pro	Gln	Gly	Asp	Ser	Met	Met	Thr	Cys	Glu	Gln	80	85	90
Ala	Gln	Leu	Leu	Ala	Asn	Leu	Ala	Arg	Leu	Ile	Gln	Ala	Lys	Lys	95	100	105
Ala	Leu	Asp	Leu	Gly	Thr	Phe	Thr	Gly	Tyr	Ser	Ala	Leu	Ala	Leu	110	115	120
Ala	Leu	Ala	Leu	Pro	Ala	Asp	Gly	Arg	Val	Val	Thr	Cys	Glu	Val	125	130	135
Asp	Ala	Gln	Pro	Pro	Glu	Leu	Gly	Arg	Pro	Leu	Trp	Arg	Gln	Ala	140	145	150
Glu	Ala	Glu	His	Lys	Ile	Asp	Leu	Arg	Leu	Lys	Pro	Ala	Leu	Glu	155	160	165
Thr	Leu	Asp	Glu	Leu	Leu	Ala	Ala	Gly	Glu	Ala	Gly	Thr	Phe	Asp	170	175	180
Val	Ala	Val	Val	Asp	Ala	Asp	Lys	Glu	Asn	Cys	Ser	Ala	Tyr	Tyr	185	190	195
Glu	Arg	Cys	Leu	Gln	Leu	Leu	Arg	Pro	Gly	Gly	Ile	Leu	Ala	Val	200	205	210
Leu	Arg	Val	Leu	Trp	Arg	Gly	Lys	Val	Leu	Gln	Pro	Pro	Lys	Gly	215	220	225
Asp	Val	Ala	Ala	Glu	Cys	Val	Arg	Asn	Leu	Asn	Glu	Arg	Ile	Arg	230	235	240
Arg	Asp	Val	Arg	Val	Tyr	Ile	Ser	Leu	Leu	Pro	Leu	Gly	Asp	Gly	245	250	255
Leu	Thr	Leu	Ala	Phe	Lys	Ile									260		

<210> 307  
 <211> 2272  
 <212> DNA  
 <213> Homo sapiens

<400> 307  
 ccgccgccgc agccgctacc gccgctgcag ccgctttccg cggcctgggc 50  
 ctctcgccgt cagcatgccca cagccttca agcccgggga cttggtgttc 100  
 gctaagatga agggctaccc tctactggcct gccaggatcg acgacatcgc 150  
 ggatggcgcc gtgaagcccc caccacaaca gtaccccatc tttttctttg 200  
 gcacacacga aacagccttc ctgggaccca aggacctgtt cccctacgac 250

aaatgtaaag acaagtacgg gaagcccaac aagaggaaag gcttcaatga 300  
 agggctgtgg gagatccaga acaaccccc aagcagctac agcgcctc 350  
 cgccagttag ctctccgac agcagggccc ccgaggccaa ccccgccgac 400  
 ggcagttagc ctgacgagga cgatgaggac cgggggggtca tggccgtcac 450  
 agcggtaacc gccacagctg ccagcgacag gatggagagc gactcagact 500  
 cagacaagag tagcgacaac agtggcctga agaggaagac gcctgcgcta 550  
 aagatgtcgg tctcgaaacg agcccgaag gcctccagcg acctggatca 600  
 ggccagcgtg tccccatccg aagaggagaa ctcggaagc tcatctgagt 650  
 cggagaagac cagcgaccag gacttcacac ctgagaagaa agcagcggtc 700  
 cgggcgccac ggagggggccc tctgggggga cggaaaaaa agaaggcgcc 750  
 gtcagcctcc gactccgact ccaaggccga ttcggacggg gccaagcctg 800  
 agccggtggc catggcgcg tggcgctcct cctcctcctc ttctcctcc 850  
 tctccgact ccgatgtgtc tgtgaagaag cctccgaggg gcaggaagcc 900  
 agcggagaag cctctccga agccgcgagg gcggaaccg aagcctgaac 950  
 ggcctccgtc cagctccagc agtgacagtg acagcgacga ggtggaccgc 1000  
 atcagttagt ggaagcggcg ggacgaggcg cggaggcgcg agctggaggc 1050  
 ccggcgcgcg cgagagcagg aggaggagct gcggcgccctg cgggagcagg 1100  
 agaaggagga gaaggagcgg aggcgcgagc gggccgaccg cggggaggct 1150  
 gagcggggca gcggcggcag cagcggggac gagctcaggg aggacgatga 1200  
 gcccgtcaag aagcggggac gcaagggccg gggccgggggt cccccgtcct 1250  
 cctctgactc cgagcccgag gccgagctgg agagagaggc caagaaatca 1300  
 gcgaagaagc cgagtcctc aagcacagag cccgccagga aacctggcca 1350  
 gaaggagaag agagtgcggc ccgaggagaa gcaacaagcc aagcccgtga 1400  
 aggtggagcg gacccggaag cggtcgagg gcttctcgat ggacaggaag 1450  
 gtagagaaga agaaagagcc ctccgtggag gagaagctgc agaagctgca 1500  
 cagttagatc aagtttggc taaaggctga cagcccgac gtgaagaggt 1550  
 gcctgaatgc cctagaggag ctgggaaccc tgcaggtgac ctctcagatc 1600  
 ctccagaaga acacagacgt ggtggccacc ttgaagaaga ttgcccgtta 1650  
 caaagcgaac aaggacgtaa tggagaaggc agcagaagtc tatacccggc 1700

tcaagtcgcg ggtcctcggc ccaaagatcg aggcgggtgca gaaagtgaac 1750  
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gctggccggg gaggaggccc ccaggagaa ggcggaggac aagcccagca 1850  
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agcgcagagg acaaggagca cgaggagggt cgggactcgg aggagggggc 1950  
aaggtgtggc tcctctgaag acctgcacga cagcgtacgg gaggggtccg 2000  
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gcagagcaga gaactgtggg gaacgctgtg ctgtttgtat ttgttccctt 2200  
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actataaacg gttttttaat ga 2272

<210> 308  
<211> 671  
<212> PRT  
<213> Homo sapiens

<400> 308  
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Gly Ala Val Lys Pro Pro Pro Asn Lys Tyr Pro Ile Phe Phe Phe  
35 40 45  
Gly Thr His Glu Thr Ala Phe Leu Gly Pro Lys Asp Leu Phe Pro  
50 55 60  
Tyr Asp Lys Cys Lys Asp Lys Tyr Gly Lys Pro Asn Lys Arg Lys  
65 70 75  
Gly Phe Asn Glu Gly Leu Trp Glu Ile Gln Asn Asn Pro His Ala  
80 85 90  
Ser Tyr Ser Ala Pro Pro Pro Val Ser Ser Ser Asp Ser Glu Ala  
95 100 105  
Pro Glu Ala Asn Pro Ala Asp Gly Ser Asp Ala Asp Glu Asp Asp  
110 115 120  
Glu Asp Arg Gly Val Met Ala Val Thr Ala Val Thr Ala Thr Ala  
125 130 135  
Ala Ser Asp Arg Met Glu Ser Asp Ser Asp Ser Asp Lys Ser Ser

	140		145		150
Asp Asn Ser Gly	Leu Lys Arg Lys Thr	Pro Ala Leu Lys Met	Ser		
	155	160	165		
Val Ser Lys Arg	Ala Arg Lys Ala Ser	Ser Asp Leu Asp Gln	Ala		
	170	175	180		
Ser Val Ser Pro	Ser Glu Glu Glu Asn	Ser Glu Ser Ser Ser	Glu		
	185	190	195		
Ser Glu Lys Thr	Ser Asp Gln Asp Phe	Thr Pro Glu Lys Lys	Ala		
	200	205	210		
Ala Val Arg Ala	Pro Arg Arg Gly Pro	Leu Gly Gly Arg Lys	Lys		
	215	220	225		
Lys Lys Ala Pro	Ser Ala Ser Asp Ser	Asp Ser Lys Ala Asp	Ser		
	230	235	240		
Asp Gly Ala Lys	Pro Glu Pro Val Ala	Met Ala Arg Ser Ala	Ser		
	245	250	255		
Ser Ser Ser Ser	Ser Ser Ser Ser Ser	Asp Ser Asp Val Ser	Val		
	260	265	270		
Lys Lys Pro Pro	Arg Gly Arg Lys Pro	Ala Glu Lys Pro Leu	Pro		
	275	280	285		
Lys Pro Arg Gly	Arg Lys Pro Lys Pro	Glu Arg Pro Pro Ser	Ser		
	290	295	300		
Ser Ser Ser Asp	Ser Asp Ser Asp Glu	Val Asp Arg Ile Ser	Glu		
	305	310	315		
Trp Lys Arg Arg	Asp Glu Ala Arg Arg	Arg Glu Leu Glu Ala	Arg		
	320	325	330		
Arg Arg Arg Glu	Gln Glu Glu Glu Leu	Arg Arg Leu Arg Glu	Gln		
	335	340	345		
Glu Lys Glu Glu	Lys Glu Arg Arg Arg	Glu Arg Ala Asp Arg	Gly		
	350	355	360		
Glu Ala Glu Arg	Gly Ser Gly Gly Ser	Ser Gly Asp Glu Leu	Arg		
	365	370	375		
Glu Asp Asp Glu	Pro Val Lys Lys Arg	Gly Arg Lys Gly Arg	Gly		
	380	385	390		
Arg Gly Pro Pro	Ser Ser Ser Asp Ser	Glu Pro Glu Ala Glu	Leu		
	395	400	405		
Glu Arg Glu Ala	Lys Lys Ser Ala Lys	Lys Pro Gln Ser Ser	Ser		
	410	415	420		
Thr Glu Pro Ala	Arg Lys Pro Gly Gln	Lys Glu Lys Arg Val	Arg		
	425	430	435		

Pro Glu Glu Lys Gln Gln Ala Lys Pro Val Lys Val Glu Arg Thr  
440 445 450

Arg Lys Arg Ser Glu Gly Phe Ser Met Asp Arg Lys Val Glu Lys  
455 460 465

Lys Lys Glu Pro Ser Val Glu Glu Lys Leu Gln Lys Leu His Ser  
470 475 480

Glu Ile Lys Phe Ala Leu Lys Val Asp Ser Pro Asp Val Lys Arg  
485 490 495

Cys Leu Asn Ala Leu Glu Glu Leu Gly Thr Leu Gln Val Thr Ser  
500 505 510

Gln Ile Leu Gln Lys Asn Thr Asp Val Val Ala Thr Leu Lys Lys  
515 520 525

Ile Arg Arg Tyr Lys Ala Asn Lys Asp Val Met Glu Lys Ala Ala  
530 535 540

Glu Val Tyr Thr Arg Leu Lys Ser Arg Val Leu Gly Pro Lys Ile  
545 550 555

Glu Ala Val Gln Lys Val Asn Lys Ala Gly Met Glu Lys Glu Lys  
560 565 570

Ala Glu Glu Lys Leu Ala Gly Glu Glu Leu Ala Gly Glu Glu Ala  
575 580 585

Pro Gln Glu Lys Ala Glu Asp Lys Pro Ser Thr Asp Leu Ser Ala  
590 595 600

Pro Val Asn Gly Glu Ala Thr Ser Gln Lys Gly Glu Ser Ala Glu  
605 610 615

Asp Lys Glu His Glu Glu Gly Arg Asp Ser Glu Glu Gly Pro Arg  
620 625 630

Cys Gly Ser Ser Glu Asp Leu His Asp Ser Val Arg Glu Gly Pro  
635 640 645

Asp Leu Asp Arg Pro Gly Ser Asp Arg Gln Glu Arg Glu Arg Ala  
650 655 660

Arg Gly Asp Ser Glu Ala Leu Asp Glu Glu Ser  
665 670

<210> 309  
<211> 3871  
<212> DNA  
<213> Homo sapiens

<400> 309  
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cagcctcaat aattatatta aattaacacc atttgaaaga gaacattggt 100







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 atattttaat aaaacaagga aaacataatg atgtataatg catcctgatg 3250  
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 aagagtagac attttattta taaccaatga tatttcagta tatattttct 3550  
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 ataaataagc ctgctacatg t 3871

<210> 310  
 <211> 777  
 <212> PRT  
 <213> Homo sapiens

<400> 310  
 Met Asn Ala Asn Lys Asp Glu Arg Leu Lys Ala Arg Ser Gln Asp  
 1 5 10 15  
 Phe His Leu Phe Pro Ala Leu Met Met Leu Ser Met Thr Met Leu  
 20 25 30  
 Phe Leu Pro Val Thr Gly Thr Leu Lys Gln Asn Ile Pro Arg Leu  
 35 40 45  
 Lys Leu Thr Tyr Lys Asp Leu Leu Leu Ser Asn Ser Cys Ile Pro  
 50 55 60  
 Phe Leu Gly Ser Ser Glu Gly Leu Asp Phe Gln Thr Leu Leu Leu  
 65 70 75  
 Asp Glu Glu Arg Gly Arg Leu Leu Leu Gly Ala Lys Asp His Ile

80										85					90				
Phe	Leu	Leu	Ser	Leu	Val	Asp	Leu	Asn	Lys	Asn	Phe	Lys	Lys	Ile					
				95					100					105					
Tyr	Trp	Pro	Ala	Ala	Lys	Glu	Arg	Val	Glu	Leu	Cys	Lys	Leu	Ala					
				110					115					120					
Gly	Lys	Asp	Ala	Asn	Thr	Glu	Cys	Ala	Asn	Phe	Ile	Arg	Val	Leu					
				125					130					135					
Gln	Pro	Tyr	Asn	Lys	Thr	His	Ile	Tyr	Val	Cys	Gly	Thr	Gly	Ala					
				140					145					150					
Phe	His	Pro	Ile	Cys	Gly	Tyr	Ile	Asp	Leu	Gly	Val	Tyr	Lys	Glu					
				155					160					165					
Asp	Ile	Ile	Phe	Lys	Leu	Asp	Thr	His	Asn	Leu	Glu	Ser	Gly	Arg					
				170					175					180					
Leu	Lys	Cys	Pro	Phe	Asp	Pro	Gln	Gln	Pro	Phe	Ala	Ser	Val	Met					
				185					190					195					
Thr	Asp	Glu	Tyr	Leu	Tyr	Ser	Gly	Thr	Ala	Ser	Asp	Phe	Leu	Gly					
				200					205					210					
Lys	Asp	Thr	Ala	Phe	Thr	Arg	Ser	Leu	Gly	Pro	Thr	His	Asp	His					
				215					220					225					
His	Tyr	Ile	Arg	Thr	Asp	Ile	Ser	Glu	His	Tyr	Trp	Leu	Asn	Gly					
				230					235					240					
Ala	Lys	Phe	Ile	Gly	Thr	Phe	Phe	Ile	Pro	Asp	Thr	Tyr	Asn	Pro					
				245					250					255					
Asp	Asp	Asp	Lys	Ile	Tyr	Phe	Phe	Phe	Arg	Glu	Ser	Ser	Gln	Glu					
				260					265					270					
Gly	Ser	Thr	Ser	Asp	Lys	Thr	Ile	Leu	Ser	Arg	Val	Gly	Arg	Val					
				275					280					285					
Cys	Lys	Asn	Asp	Val	Gly	Gly	Gln	Arg	Ser	Leu	Ile	Asn	Lys	Trp					
				290					295					300					
Thr	Thr	Phe	Leu	Lys	Ala	Arg	Leu	Ile	Cys	Ser	Ile	Pro	Gly	Ser					
				305					310					315					
Asp	Gly	Ala	Asp	Thr	Tyr	Phe	Asp	Glu	Leu	Gln	Asp	Ile	Tyr	Leu					
				320					325					330					
Leu	Pro	Thr	Arg	Asp	Glu	Arg	Asn	Pro	Val	Val	Tyr	Gly	Val	Phe					
				335					340					345					
Thr	Thr	Thr	Ser	Ser	Ile	Phe	Lys	Gly	Ser	Ala	Val	Cys	Val	Tyr					
				350					355					360					
Ser	Met	Ala	Asp	Ile	Arg	Ala	Val	Phe	Asn	Gly	Pro	Tyr	Ala	His					
				365					370					375					

Lys Glu Ser Ala	Asp His Arg Trp Val	Gln Tyr Asp Gly Arg	Ile
380		385	390
Pro Tyr Pro Arg	Pro Gly Thr Cys Pro	Ser Lys Thr Tyr Asp	Pro
395		400	405
Leu Ile Lys Ser	Thr Arg Asp Phe Pro	Asp Asp Val Ile Ser	Phe
410		415	420
Ile Lys Arg His	Ser Val Met Tyr Lys	Ser Val Tyr Pro Val	Ala
425		430	435
Gly Gly Pro Thr	Phe Lys Arg Ile Asn	Val Asp Tyr Arg Leu	Thr
440		445	450
Gln Ile Val Val	Asp His Val Ile Ala	Glu Asp Gly Gln Tyr	Asp
455		460	465
Val Met Phe Leu	Gly Thr Asp Ile Gly	Thr Val Leu Lys Val	Val
470		475	480
Ser Ile Ser Lys	Glu Lys Trp Asn Met	Glu Glu Val Val Leu	Glu
485		490	495
Glu Leu Gln Ile	Phe Lys His Ser Ser	Ile Ile Leu Asn Met	Glu
500		505	510
Leu Ser Leu Lys	Gln Gln Gln Leu Tyr	Ile Gly Ser Arg Asp	Gly
515		520	525
Leu Val Gln Leu	Ser Leu His Arg Cys	Asp Thr Tyr Gly Lys	Ala
530		535	540
Cys Ala Asp Cys	Cys Leu Ala Arg Asp	Pro Tyr Cys Ala Trp	Asp
545		550	555
Gly Asn Ala Cys	Ser Arg Tyr Ala Pro	Thr Ser Lys Arg Arg	Ala
560		565	570
Arg Arg Gln Asp	Val Lys Tyr Gly Asp	Pro Ile Thr Gln Cys	Trp
575		580	585
Asp Ile Glu Asp	Ser Ile Ser His Glu	Thr Ala Asp Glu Lys	Val
590		595	600
Ile Phe Gly Ile	Glu Phe Asn Ser Thr	Phe Leu Glu Cys Ile	Pro
605		610	615
Lys Ser Gln Gln	Ala Thr Ile Lys Trp	Tyr Ile Gln Arg Ser	Gly
620		625	630
Asp Glu His Arg	Glu Glu Leu Lys Pro	Asp Glu Arg Ile Ile	Lys
635		640	645
Thr Glu Tyr Gly	Leu Leu Ile Arg Ser	Leu Gln Lys Lys Asp	Ser
650		655	660
Gly Met Tyr Tyr	Cys Lys Ala Gln Glu	His Thr Phe Ile His	Thr

	665		670		675
Ile Val Lys Leu	Thr Leu Asn Val Ile	Glu Asn Glu Gln Met Glu			
	680	685		690	
Asn Thr Gln Arg	Ala Glu His Glu Glu	Gly Gln Val Lys Asp Leu			
	695	700		705	
Leu Ala Glu Ser	Arg Leu Arg Tyr Lys	Asp Tyr Ile Gln Ile Leu			
	710	715		720	
Ser Ser Pro Asn	Phe Ser Leu Asp Gln	Tyr Cys Glu Gln Met Trp			
	725	730		735	
His Arg Glu Lys	Arg Arg Gln Arg Asn	Lys Gly Gly Pro Lys Trp			
	740	745		750	
Lys His Met Gln	Glu Met Lys Lys Lys	Arg Asn Arg Arg His His			
	755	760		765	
Arg Asp Leu Asp	Glu Leu Pro Arg Ala	Val Ala Thr			
	770	775			

<210> 311  
 <211> 25  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-25  
 <223> Synthetic construct.

<400> 311  
 caacgcagcc gtgataaaca agtgg 25

<210> 312  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 312  
 gcttggacat gtaccaggcc gtgg 24

<210> 313  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 313  
ggccagactg atttgctcaa ttccctggaag tgatggggca gatac 45

<210> 314  
<211> 3934  
<212> DNA  
<213> Homo sapiens

<400> 314  
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agacctgaag ctgtttcttc aggagcctgg tgtattttcc cccacccac 150  
ctcagcagtt tcagccagca gggactgac aggtgtgtgt cctggagtgg 200  
ggagcagaag gcgtggctgg caagagtggc ctggagaaag aggttcagcg 250  
cttgaccagc cgagctgccc gtgactacaa gatccagaac catgggcatc 300  
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gaagagctga gagaggggat cttggagcca ttgaggggtgt catggagcta 400  
cagaggggag ggaaaggtat ttttaaggtaa cagtgtggca caatagttaa 450  
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tatttccacc ctcacctcca aggggtgaaa cttgcccctt cccatttcta 1900  
gagctggaac ccactccttt ttttcccatt gttctatcat ctctaggacc 1950  
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cctgaaatct ctggggctgg aaaccatcca tcaaggcttc tagtagttct 2050  
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<210> 315

<211> 370

<212> PRT

<213> Homo sapiens

<400> 315

Met	Gln	Leu	Ala	Lys	Tyr	Gln	Ser	His	Ser	Lys	Ser	Cys	Pro	Thr
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Val	Phe	Pro	Pro	Thr	Pro	Val	Leu	Cys	Leu	Pro	Asn	Gln	Val	Leu		20	25	30
Gln	Arg	Leu	Glu	Gln	Arg	Arg	Gln	Gln	Ala	Ser	Glu	Arg	Glu	Ala		35	40	45
Pro	Ser	Ile	Glu	Gln	Arg	Leu	Gln	Glu	Val	Arg	Glu	Ser	Ile	Arg		50	55	60
Arg	Ala	Gln	Val	Ser	Gln	Val	Lys	Gly	Ala	Ala	Arg	Leu	Ala	Leu		65	70	75
Leu	Gln	Gly	Ala	Gly	Leu	Asp	Val	Glu	Arg	Trp	Leu	Lys	Pro	Ala		80	85	90
Met	Thr	Gln	Ala	Gln	Asp	Glu	Val	Glu	Gln	Glu	Arg	Arg	Leu	Ser		95	100	105
Glu	Ala	Arg	Leu	Ser	Gln	Arg	Asp	Leu	Ser	Pro	Thr	Ala	Glu	Asp		110	115	120
Ala	Glu	Leu	Ser	Asp	Phe	Glu	Glu	Cys	Glu	Glu	Thr	Gly	Glu	Leu		125	130	135
Phe	Glu	Glu	Pro	Ala	Pro	Gln	Ala	Leu	Ala	Thr	Arg	Ala	Leu	Pro		140	145	150
Cys	Pro	Ala	His	Val	Val	Phe	Arg	Tyr	Gln	Ala	Gly	Arg	Glu	Asp		155	160	165
Glu	Leu	Thr	Ile	Thr	Glu	Gly	Glu	Trp	Leu	Glu	Val	Ile	Glu	Glu		170	175	180
Gly	Asp	Ala	Asp	Glu	Trp	Val	Lys	Ala	Arg	Asn	Gln	His	Gly	Glu		185	190	195
Val	Gly	Phe	Val	Pro	Glu	Arg	Tyr	Leu	Asn	Phe	Pro	Asp	Leu	Ser		200	205	210
Leu	Pro	Glu	Ser	Ser	Gln	Asp	Ser	Asp	Asn	Pro	Cys	Gly	Ala	Glu		215	220	225
Pro	Thr	Ala	Phe	Leu	Ala	Gln	Ala	Leu	Tyr	Ser	Tyr	Thr	Gly	Gln		230	235	240
Ser	Ala	Glu	Glu	Leu	Ser	Phe	Pro	Glu	Gly	Ala	Leu	Ile	Arg	Leu		245	250	255
Leu	Pro	Arg	Ala	Gln	Asp	Gly	Val	Asp	Asp	Gly	Phe	Trp	Arg	Gly		260	265	270
Glu	Phe	Gly	Gly	Arg	Val	Gly	Val	Phe	Pro	Ser	Leu	Leu	Val	Glu		275	280	285
Glu	Leu	Leu	Gly	Pro	Pro	Gly	Pro	Pro	Glu	Leu	Ser	Asp	Pro	Glu		290	295	300
Gln	Met	Leu	Pro	Ser	Pro	Ser	Pro	Pro	Ser	Phe	Ser	Pro	Pro	Ala				



305	310	315
Pro Thr Ser Val	Leu Asp Gly Pro Pro	Ala Pro Val Leu Pro Gly
320	325	330
Asp Lys Ala Leu	Asp Phe Pro Gly Phe	Leu Asp Met Met Ala Pro
335	340	345
Arg Leu Arg Pro	Met Arg Pro Pro Pro	Pro Pro Pro Ala Lys Ala
350	355	360
Pro Asp Pro Gly	His Pro Asp Pro Leu Thr	
365	370	

<210> 316  
 <211> 4407  
 <212> DNA  
 <213> Homo sapiens

<400> 316  
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 agacagagac aaaggcacag cggaagaagg cagagacagg gcaggcacag 100  
 aagcggccca gacagagtcc tacagagggg gagggccagag aagctgcaga 150  
 agacacaggc agggagagac aaagatccag gaaaggaggg ctcaggagga 200  
 gagtttgag aagccagacc cctgggcacc tctcccaagc ccaaggacta 250  
 agttttctcc atttccttta acggctctca gcccttctga aaactttgcc 300  
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 aaagctaggg tgtggaggac ttggtgccct agaaggcctc agtccctccc 400  
 agctgcagta ccagtgccat gtcccagaca ggctcgcac cggggagggg 450  
 cttggcaggg cgctggctgt ggggagccca accctgcctc ctgctcccca 500  
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 cgtgtttcca gagaagctca acggcagcgt cctgcctggc tcgggcgccc 650  
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ccaataataa tacctccctt agaagtttgt tgtgaggatt aaataatgta 4300  
aataaagaac tagcataaca ctcaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4350  
aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 4400  
aaggaaa 4407

<210> 317  
<211> 837  
<212> PRT  
<213> Homo sapiens

<400> 317  
Met Ser Gln Thr Gly Ser His Pro Gly Arg Gly Leu Ala Gly Arg  
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Trp Leu Trp Gly Ala Gln Pro Cys Leu Leu Leu Pro Ile Val Pro  
20 25 30  
Leu Ser Trp Leu Val Trp Leu Leu Leu Leu Leu Ala Ser Leu  
35 40 45  
Leu Pro Ser Ala Arg Leu Ala Ser Pro Leu Pro Arg Glu Glu Glu  
50 55 60  
Ile Val Phe Pro Glu Lys Leu Asn Gly Ser Val Leu Pro Gly Ser  
65 70 75  
Gly Ala Pro Ala Arg Leu Leu Cys Arg Leu Gln Ala Phe Gly Glu  
80 85 90  
Thr Leu Leu Leu Glu Leu Glu Gln Asp Ser Gly Val Gln Val Glu  
95 100 105  
Gly Leu Thr Val Gln Tyr Leu Gly Gln Ala Pro Glu Leu Leu Gly  
110 115 120  
Gly Ala Glu Pro Gly Thr Tyr Leu Thr Gly Thr Ile Asn Gly Asp  
125 130 135  
Pro Glu Ser Val Ala Ser Leu His Trp Asp Gly Gly Ala Leu Leu

	140		145		150
Gly Val Leu Gln Tyr Arg Gly Ala Glu Leu His Leu Gln Pro Leu	155		160		165
Glu Gly Gly Thr Pro Asn Ser Ala Gly Gly Pro Gly Ala His Ile	170		175		180
Leu Arg Arg Lys Ser Pro Ala Ser Gly Gln Gly Pro Met Cys Asn	185		190		195
Val Lys Ala Pro Leu Gly Ser Pro Ser Pro Arg Pro Arg Arg Ala	200		205		210
Lys Arg Phe Ala Ser Leu Ser Arg Phe Val Glu Thr Leu Val Val	215		220		225
Ala Asp Asp Lys Met Ala Ala Phe His Gly Ala Gly Leu Lys Arg	230		235		240
Tyr Leu Leu Thr Val Met Ala Ala Ala Ala Lys Ala Phe Lys His	245		250		255
Pro Ser Ile Arg Asn Pro Val Ser Leu Val Val Thr Arg Leu Val	260		265		270
Ile Leu Gly Ser Gly Glu Glu Gly Pro Gln Val Gly Pro Ser Ala	275		280		285
Ala Gln Thr Leu Arg Ser Phe Cys Ala Trp Gln Arg Gly Leu Asn	290		295		300
Thr Pro Glu Asp Ser Gly Pro Asp His Phe Asp Thr Ala Ile Leu	305		310		315
Phe Thr Arg Gln Asp Leu Cys Gly Val Ser Thr Cys Asp Thr Leu	320		325		330
Gly Met Ala Asp Val Gly Thr Val Cys Asp Pro Ala Arg Ser Cys	335		340		345
Ala Ile Val Glu Asp Asp Gly Leu Gln Ser Ala Phe Thr Ala Ala	350		355		360
His Glu Leu Gly His Val Phe Asn Met Leu His Asp Asn Ser Lys	365		370		375
Pro Cys Ile Ser Leu Asn Gly Pro Leu Ser Thr Ser Arg His Val	380		385		390
Met Ala Pro Val Met Ala His Val Asp Pro Glu Glu Pro Trp Ser	395		400		405
Pro Cys Ser Ala Arg Phe Ile Thr Asp Phe Leu Asp Asn Gly Tyr	410		415		420
Gly His Cys Leu Leu Asp Lys Pro Glu Ala Pro Leu His Leu Pro	425		430		435

Val	Thr	Phe	Pro	Gly	Lys	Asp	Tyr	Asp	Ala	Asp	Arg	Gln	Cys	Gln	
				440					445					450	
Leu	Thr	Phe	Gly	Pro	Asp	Ser	Arg	His	Cys	Pro	Gln	Leu	Pro	Pro	
				455					460					465	
Pro	Cys	Ala	Ala	Leu	Trp	Cys	Ser	Gly	His	Leu	Asn	Gly	His	Ala	
				470					475					480	
Met	Cys	Gln	Thr	Lys	His	Ser	Pro	Trp	Ala	Asp	Gly	Thr	Pro	Cys	
				485					490					495	
Gly	Pro	Ala	Gln	Ala	Cys	Met	Gly	Gly	Arg	Cys	Leu	His	Met	Asp	
				500					505					510	
Gln	Leu	Gln	Asp	Phe	Asn	Ile	Pro	Gln	Ala	Gly	Gly	Trp	Gly	Pro	
				515					520					525	
Trp	Gly	Pro	Trp	Gly	Asp	Cys	Ser	Arg	Thr	Cys	Gly	Gly	Gly	Val	
				530					535					540	
Gln	Phe	Ser	Ser	Arg	Asp	Cys	Thr	Arg	Pro	Val	Pro	Arg	Asn	Gly	
				545					550					555	
Gly	Lys	Tyr	Cys	Glu	Gly	Arg	Arg	Thr	Arg	Phe	Arg	Ser	Cys	Asn	
				560					565					570	
Thr	Glu	Asp	Cys	Pro	Thr	Gly	Ser	Ala	Leu	Thr	Phe	Arg	Glu	Glu	
				575					580					585	
Gln	Cys	Ala	Ala	Tyr	Asn	His	Arg	Thr	Asp	Leu	Phe	Lys	Ser	Phe	
				590					595					600	
Pro	Gly	Pro	Met	Asp	Trp	Val	Pro	Arg	Tyr	Thr	Gly	Val	Ala	Pro	
				605					610					615	
Gln	Asp	Gln	Cys	Lys	Leu	Thr	Cys	Gln	Ala	Arg	Ala	Leu	Gly	Tyr	
				620					625					630	
Tyr	Tyr	Val	Leu	Glu	Pro	Arg	Val	Val	Asp	Gly	Thr	Pro	Cys	Ser	
				635					640					645	
Pro	Asp	Ser	Ser	Ser	Val	Cys	Val	Gln	Gly	Arg	Cys	Ile	His	Ala	
				650					655					660	
Gly	Cys	Asp	Arg	Ile	Ile	Gly	Ser	Lys	Lys	Lys	Phe	Asp	Lys	Cys	
				665					670					675	
Met	Val	Cys	Gly	Gly	Asp	Gly	Ser	Gly	Cys	Ser	Lys	Gln	Ser	Gly	
				680					685					690	
Ser	Phe	Arg	Lys	Phe	Arg	Tyr	Gly	Tyr	Asn	Asn	Val	Val	Thr	Ile	
				695					700					705	
Pro	Ala	Gly	Ala	Thr	His	Ile	Leu	Val	Arg	Gln	Gln	Gly	Asn	Pro	
				710					715					720	
Gly	His	Arg	Ser	Ile	Tyr	Leu	Ala	Leu	Lys	Leu	Pro	Asp	Gly	Ser	

725	730	735
Tyr Ala Leu Asn Gly Glu Tyr Thr Leu Met Pro Ser Pro Thr Asp		
740	745	750
Val Val Leu Pro Gly Ala Val Ser Leu Arg Tyr Ser Gly Ala Thr		
755	760	765
Ala Ala Ser Glu Thr Leu Ser Gly His Gly Pro Leu Ala Gln Pro		
770	775	780
Leu Thr Leu Gln Val Leu Val Ala Gly Asn Pro Gln Asp Thr Arg		
785	790	795
Leu Arg Tyr Ser Phe Phe Val Pro Arg Pro Thr Pro Ser Thr Pro		
800	805	810
Arg Pro Thr Pro Gln Asp Trp Leu His Arg Arg Ala Gln Ile Leu		
815	820	825
Glu Ile Leu Arg Arg Arg Pro Trp Ala Gly Arg Lys		
830	835	

<210> 318  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 318  
 ccctgaagct gccagatggc tcc 23

<210> 319  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 319  
 ctgtgctctt cgggtgcagcc agtc 24

<210> 320  
 <211> 43  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-43  
 <223> Synthetic construct.

<400> 320  
ccacagatgt ggtactgcct ggggcagtca gcttgogcta cag 43

<210> 321  
<211> 1197  
<212> DNA  
<213> Homo sapiens

<400> 321  
cagcagtggg ctctcagtc tctcaaagca aggaaagagt actgtgtgct 50  
gagagaccat ggcaaagaat cctccagaga attgtgaaga ctgtcacatt 100  
ctaaatgcag aagcttttaa atccaagaaa atatgtaaat cacttaagat 150  
ttgtggactg gtgttttgta tcctggccct aactctaatt gtcctgtttt 200  
gggggagcaa gcacttctgg ccggagggtac ccaaaaaagc ctatgacatg 250  
gagcacactt tctacagcaa tggagagaag aagaagattt acatggaaat 300  
tgatcctgtg accagaactg aaatatcag aagcggaaat ggcactgatg 350  
aaacattgga agtgcacgac tttaaaaacg gatacactgg catctacttc 400  
gtgggtcttc aaaaatgttt tatcaaaact cagattaaag tgattcctga 450  
atcttctgaa ccagaagagg aaatagatga gaatgaagaa attaccacaa 500  
ctttctttga acagtcagtg atttgggtcc cagcagaaaa gcctattgaa 550  
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gaccatgtat tggatcaatc ccactcta atcagtttct gagttacaag 650  
actttgagga ggaggagaa gatcttact ttctgccaa cgaaaaaaaa 700  
gggattgaac aaaatgaaca gtgggtgggc cctcaagtga aagtagagaa 750  
gaccgcgtcac gccagacaag caagtgagga agaacttcca ataatgact 800  
atactgaaaa tggaatagaa tttgatccca tgctggatga gagaggttat 850  
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tcctctgtcg tgcctcatg ccttgtaact ggtgggtggc ccgcatgctg 1000  
gggaggggtct aataggaggt ttgagctcaa atgcttaaac tgctggcaac 1050  
atataataaa tgcctgctat tcaatgaatt tctgcctatg aggcctctgg 1100  
cccctggtag ccagctctcc agaattactt gtaggtaatt cctctcttca 1150  
tgttctaata aacttctaca ttatcaccaa aaaaaaaaaa aaaaaaa 1197

<210> 322



<211> 317  
 <212> PRT  
 <213> Homo sapiens

<400> 322

Met	Ala	Lys	Asn	Pro	Pro	Glu	Asn	Cys	Glu	Asp	Cys	His	Ile	Leu	
1				5					10					15	
Asn	Ala	Glu	Ala	Phe	Lys	Ser	Lys	Lys	Ile	Cys	Lys	Ser	Leu	Lys	
				20					25					30	
Ile	Cys	Gly	Leu	Val	Phe	Gly	Ile	Leu	Ala	Leu	Thr	Leu	Ile	Val	
				35					40					45	
Leu	Phe	Trp	Gly	Ser	Lys	His	Phe	Trp	Pro	Glu	Val	Pro	Lys	Lys	
				50					55					60	
Ala	Tyr	Asp	Met	Glu	His	Thr	Phe	Tyr	Ser	Asn	Gly	Glu	Lys	Lys	
				65					70					75	
Lys	Ile	Tyr	Met	Glu	Ile	Asp	Pro	Val	Thr	Arg	Thr	Glu	Ile	Phe	
				80					85					90	
Arg	Ser	Gly	Asn	Gly	Thr	Asp	Glu	Thr	Leu	Glu	Val	His	Asp	Phe	
				95					100					105	
Lys	Asn	Gly	Tyr	Thr	Gly	Ile	Tyr	Phe	Val	Gly	Leu	Gln	Lys	Cys	
				110					115					120	
Phe	Ile	Lys	Thr	Gln	Ile	Lys	Val	Ile	Pro	Glu	Phe	Ser	Glu	Pro	
				125					130					135	
Glu	Glu	Glu	Ile	Asp	Glu	Asn	Glu	Glu	Ile	Thr	Thr	Thr	Phe	Phe	
				140					145					150	
Glu	Gln	Ser	Val	Ile	Trp	Val	Pro	Ala	Glu	Lys	Pro	Ile	Glu	Asn	
				155					160					165	
Arg	Asp	Phe	Leu	Lys	Asn	Ser	Lys	Ile	Leu	Glu	Ile	Cys	Asp	Asn	
				170					175					180	
Val	Thr	Met	Tyr	Trp	Ile	Asn	Pro	Thr	Leu	Ile	Ser	Val	Ser	Glu	
				185					190					195	
Leu	Gln	Asp	Phe	Glu	Glu	Glu	Gly	Glu	Asp	Leu	His	Phe	Pro	Ala	
				200					205					210	
Asn	Glu	Lys	Lys	Gly	Ile	Glu	Gln	Asn	Glu	Gln	Trp	Val	Val	Pro	
				215					220					225	
Gln	Val	Lys	Val	Glu	Lys	Thr	Arg	His	Ala	Arg	Gln	Ala	Ser	Glu	
				230					235					240	
Glu	Glu	Leu	Pro	Ile	Asn	Asp	Tyr	Thr	Glu	Asn	Gly	Ile	Glu	Phe	
				245					250					255	
Asp	Pro	Met	Leu	Asp	Glu	Arg	Gly	Tyr	Cys	Cys	Ile	Tyr	Cys	Arg	
				260					265					270	

Arg Gly Asn Arg Tyr Cys Arg Arg Val Cys Glu Pro Leu Leu Gly  
275 280 285

Tyr Tyr Pro Tyr Pro Tyr Cys Tyr Gln Gly Gly Arg Val Ile Cys  
290 295 300

Arg Val Ile Met Pro Cys Asn Trp Trp Val Ala Arg Met Leu Gly  
305 310 315

Arg Val

<210> 323  
<211> 1174  
<212> DNA  
<213> Homo sapiens

<400> 323  
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cagggagctg cccggctggc ctaggcaggc agccgcacca tggccagcac 100  
ggcgtgcag cttctgggct tctgctcag cttcctgggc atggtgggca 150  
cgttgatcac caccatcctg ccgactggc ggaggacagc gcacgtgggc 200  
accaacatcc tcacggccgt gtcctacctg aaagggctct ggatggagtg 250  
tgtgtggcac agcacaggca tctaccagtg ccagatctac cgatccctgc 300  
tggcgtgcc ccaagacctc caggtgccc gcgcctcat ggtcatctcc 350  
tgcctgctct cgggcatagc ctgcgcctgc gccgtcatcg ggatgaagtg 400  
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tggaccacca acgacgtggt gcagaacttc tacaaccgc tgctgccag 550  
cggcatgaag tttgagattg gccaggccct gtacctgggc ttcattctct 600  
cgtccctctc gtcattggt ggcaccctgc tttgcctgtc ctgccaggac 650  
gaggcaccct acaggcccta ccaggccccg cccagggcca ccacgaccac 700  
tgcaaacacc gcacctgcct accagccacc agctgcctac aaagacaatc 750  
gggccccctc agtgacctcg gccacgcaca gcgggtacag gctgaacgac 800  
tacgtgtgag tccccacagc ctgcttctcc cctgggctgc tgtgggctgg 850  
gtccccggcg ggactgtcaa tggaggcagg ggttccagca caaagtttac 900  
ttctgggcaa tttttgtatc caaggaaata atgtgaatgc gaggaaatgt 950  
ctttagagca caggacaga gggggaaata agaggaggag aaagctctct 1000

ataccaaaga ctgaaaaaaa aaatcctgtc tgtttttgta tttattatat 1050  
 atatttatgt ggggtgattg ataacaagtt taatataaag tgacttggga 1100  
 gtttggtcag tgggggttgggt ttgtgatcca ggaataaacc ttgcggatgt 1150  
 ggctgtttat gaaaaaaaaa aaaa 1174

<210> 324

<211> 239

<212> PRT

<213> Homo sapiens

<400> 324

Met	Ala	Ser	Thr	Ala	Val	Gln	Leu	Leu	Gly	Phe	Leu	Leu	Ser	Phe	1	5	10	15
Leu	Gly	Met	Val	Gly	Thr	Leu	Ile	Thr	Thr	Ile	Leu	Pro	His	Trp	20	25	30	
Arg	Arg	Thr	Ala	His	Val	Gly	Thr	Asn	Ile	Leu	Thr	Ala	Val	Ser	35	40	45	
Tyr	Leu	Lys	Gly	Leu	Trp	Met	Glu	Cys	Val	Trp	His	Ser	Thr	Gly	50	55	60	
Ile	Tyr	Gln	Cys	Gln	Ile	Tyr	Arg	Ser	Leu	Leu	Ala	Leu	Pro	Gln	65	70	75	
Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Met	Val	Ile	Ser	Cys	Leu	Leu	80	85	90	
Ser	Gly	Ile	Ala	Cys	Ala	Cys	Ala	Val	Ile	Gly	Met	Lys	Cys	Thr	95	100	105	
Arg	Cys	Ala	Lys	Gly	Thr	Pro	Ala	Lys	Thr	Thr	Phe	Ala	Ile	Leu	110	115	120	
Gly	Gly	Thr	Leu	Phe	Ile	Leu	Ala	Gly	Leu	Leu	Cys	Met	Val	Ala	125	130	135	
Val	Ser	Trp	Thr	Thr	Asn	Asp	Val	Val	Gln	Asn	Phe	Tyr	Asn	Pro	140	145	150	
Leu	Leu	Pro	Ser	Gly	Met	Lys	Phe	Glu	Ile	Gly	Gln	Ala	Leu	Tyr	155	160	165	
Leu	Gly	Phe	Ile	Ser	Ser	Ser	Leu	Ser	Leu	Ile	Gly	Gly	Thr	Leu	170	175	180	
Leu	Cys	Leu	Ser	Cys	Gln	Asp	Glu	Ala	Pro	Tyr	Arg	Pro	Tyr	Gln	185	190	195	
Ala	Pro	Pro	Arg	Ala	Thr	Thr	Thr	Thr	Ala	Asn	Thr	Ala	Pro	Ala	200	205	210	
Tyr	Gln	Pro	Pro	Ala	Ala	Tyr	Lys	Asp	Asn	Arg	Ala	Pro	Ser	Val	215	220	225	

Thr Ser Ala Thr His Ser Gly Tyr Arg Leu Asn Asp Tyr Val  
 230 235

<210> 325  
 <211> 2121  
 <212> DNA  
 <213> Homo sapiens

<400> 325  
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 cacatgccaa gtggtggcgt tcctcctgtc catcctgggg ctggccggct 150  
 gcatcgcggc caccgggatg gacatgtgga gcaccagga cctgtacgac 200  
 aaccccgctca cctccgtgtt ccagtacgaa gggctctgga ggagctgcgt 250  
 gaggcagagt tcaggcttca ccgaatgcag gccctatttc accatcctgg 300  
 gacttcacgc catgctgcag gcagtgcgag ccctgatgat cgtaggcatc 350  
 gtcctgggtg ccattggcct cctggatatc atctttgccc tgaaatgcat 400  
 ccgcattggc agcatggagg actctgcaa agccaacatg aactgacct 450  
 ccgggatcat gttcattgtc tcaggctctt gtgcaattgc tggagtgtct 500  
 gtgtttgcca acatgctggt gactaacttc tggatgtcca cagctaacat 550  
 gtacaccggc atgggtggga tggcgcagac tgttcagacc aggtacacat 600  
 ttggtgcggc tctgttcgtg ggctgggtcg ctggaggcct cacactaatt 650  
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 caactacaaa gccgtttctt atcatgcctc aggccacagt gttgcctaca 750  
 agcctggagg cttcaaggcc agcactggct ttgggtccaa caccaaaaac 800  
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 tccttccaag cagcactatg tgtaatgctc taagacctct cagcacgggc 900  
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 catctttgga gaggccaaat ggtottagcc tcagtctctg tctctaaata 1050  
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 attttcaatc ctctatttct ttttttaaata ataactttct actctgatga 1150  
 gagaatgtgg ttttaatctc tctctcacat tttgatgatt tagacagact 1200  
 cccctcttc ctctagtca ataaacccat tgatgatcta tttccagct 1250

tatccccaag aaaacttttg aaaggaaaga gtagacccaa agatgttatt 1300  
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 cacttactga agaagaagca ataagagaaa gatatttgta atctctccag 1400  
 cccatgatct cggtttttctt aactgtgat cttaaaagtt accaaaccaa 1450  
 agtcattttc agtttgaggc aaccaaacct ttctactgct gttgacatct 1500  
 tcttattaca gcaacaccat tctaggagtt tcctgagctc tccactggag 1550  
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 atttttttta atttaagtcc taaatatagt taaaataaat aatgttttag 1650  
 taaaatgata cactatctct gtgaaatagc ctcaccccta catgtggata 1700  
 gaaggaaatg aaaaaataat tgctttgaca ttgtctatat ggtactttgt 1750  
 aaagtcatgc ttaagtacaa attccatgaa aagctcacac ctgtaatcct 1800  
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 gactagcctg ggcaacatgg agaagccctg tctctacaaa atacagagag 1900  
 aaaaaatcag ccagtcatgg tggcatacac ctgtagtccc agcattccgg 1950  
 gaggctgagg tgggaggatc acttgagccc agggagggtt gggctgcagt 2000  
 gagccatgat cacaccactg cactccagcc aggtgacata gcgagatcct 2050  
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 aggttaaaac taattcttta a 2121

<210> 326  
 <211> 261  
 <212> PRT  
 <213> Homo sapiens

<400> 326  
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 Leu Gly Leu Ala Gly Cys Ile Ala Ala Thr Gly Met Asp Met Trp  
                     20                    25                    30  
 Ser Thr Gln Asp Leu Tyr Asp Asn Pro Val Thr Ser Val Phe Gln  
                     35                    40                    45  
 Tyr Glu Gly Leu Trp Arg Ser Cys Val Arg Gln Ser Ser Gly Phe  
                     50                    55                    60  
 Thr Glu Cys Arg Pro Tyr Phe Thr Ile Leu Gly Leu Pro Ala Met  
                     65                    70                    75  
 Leu Gln Ala Val Arg Ala Leu Met Ile Val Gly Ile Val Leu Gly

80										85					90				
Ala	Ile	Gly	Leu	Leu	Val	Ser	Ile	Phe	Ala	Leu	Lys	Cys	Ile	Arg					
				95					100					105					
Ile	Gly	Ser	Met	Glu	Asp	Ser	Ala	Lys	Ala	Asn	Met	Thr	Leu	Thr					
				110					115					120					
Ser	Gly	Ile	Met	Phe	Ile	Val	Ser	Gly	Leu	Cys	Ala	Ile	Ala	Gly					
				125					130					135					
Val	Ser	Val	Phe	Ala	Asn	Met	Leu	Val	Thr	Asn	Phe	Trp	Met	Ser					
				140					145					150					
Thr	Ala	Asn	Met	Tyr	Thr	Gly	Met	Gly	Gly	Met	Val	Gln	Thr	Val					
				155					160					165					
Gln	Thr	Arg	Tyr	Thr	Phe	Gly	Ala	Ala	Leu	Phe	Val	Gly	Trp	Val					
				170					175					180					
Ala	Gly	Gly	Leu	Thr	Leu	Ile	Gly	Gly	Val	Met	Met	Cys	Ile	Ala					
				185					190					195					
Cys	Arg	Gly	Leu	Ala	Pro	Glu	Glu	Thr	Asn	Tyr	Lys	Ala	Val	Ser					
				200					205					210					
Tyr	His	Ala	Ser	Gly	His	Ser	Val	Ala	Tyr	Lys	Pro	Gly	Gly	Phe					
				215					220					225					
Lys	Ala	Ser	Thr	Gly	Phe	Gly	Ser	Asn	Thr	Lys	Asn	Lys	Lys	Ile					
				230					235					240					
Tyr	Asp	Gly	Gly	Ala	Arg	Thr	Glu	Asp	Glu	Val	Gln	Ser	Tyr	Pro					
				245					250					255					
Ser	Lys	His	Asp	Tyr	Val														
				260															

<210> 327  
 <211> 2010  
 <212> DNA  
 <213> Homo sapiens

<400> 327  
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 caacccatgc cttagaaatc gctgggctgt ttcttggtgg tgttggaatg 150  
 gtgggcacag tggctgtcac tgatcatgct cagtggagag tgcggcctt 200  
 cattgaaaac aacatcgtgg tttttgaaaa cttctgggaa ggactgtgga 250  
 tgaattgctg gaggcaggct aacatcagga tgcagtgcaa aatctatgat 300  
 tccctgctgg ctctttctcc ggacctacag gcagccagag gactgatgtg 350

tgctgcttcc gtgatgtcct tcttggtttt catgatggcc atccttgcca 400  
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 ctgctgacgg ctggaatcat cttcatcatc acgggcatgg tgggtgctcat 500  
 ccctgtgagc tgggttgcca atgcatcatc cagagatttc tataactcaa 550  
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 tactccagaa gtcagtatgt gtagtttgtt atgttttttt aactttacta 800  
 taaagccatg caaatgacaa aaatctatat tacttttctc aaatggaccc 850  
 caaagaaact ttgattttact gttcttaact gcctaattctt aattacagga 900  
 actgtgcac agctattttat gattctataa gctatttcag cagaatgaga 950  
 tattaaacc aatgctttga ttgttctaga aagtatagta atttgttttc 1000  
 taaggtggtt caagcatcta ctctttttat catttacttc aaaatgacat 1050  
 tgctaaagac tgcattatth tactactgta atttctccac gacatagcat 1100  
 tatgtacata gatgagtgtg acattttatat ctcacataga gacatgctta 1150  
 tatggtttta tttaaaatga aatgccagtc cattacactg aataaataga 1200  
 actcaactat tgcttttcag ggaaatcatg gataggggtg aagaagggtta 1250  
 ctattaattg tttaaaaaca gcttagggat taatgtcctc catttataat 1300  
 gaagattaaa atgaaggcct taatcagcat tgtaaaggaa attgaatggc 1350  
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 atcctcttct cccagaggct ttttttttct tgtgtattaa attaacattt 1450  
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 agggctatac tcagaagaaa gataaaagtg tgatctaaga aaaagtgatg 1550  
 gtttttaggaa agtgaaaata tttttgtttt tgtatttgaa gaagaatgat 1600  
 gcattttgac aagaaatcat atatgtatgg atatatttta ataagtattt 1650  
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atTTTTgttc tgtgaaaaat aaatttcctt cttgtaccat ttctgttttag 1850  
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 tgaaactgac aatccaattt gaaagtttgt gtcgacgtct gtctagctta 1950  
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 ttttctaatt 2010

<210> 328  
 <211> 225  
 <212> PRT  
 <213> Homo sapiens

<400> 328  
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 35 40 45  
 Phe Trp Glu Gly Leu Trp Met Asn Cys Val Arg Gln Ala Asn Ile  
 50 55 60  
 Arg Met Gln Cys Lys Ile Tyr Asp Ser Leu Leu Ala Leu Ser Pro  
 65 70 75  
 Asp Leu Gln Ala Ala Arg Gly Leu Met Cys Ala Ala Ser Val Met  
 80 85 90  
 Ser Phe Leu Ala Phe Met Met Ala Ile Leu Gly Met Lys Cys Thr  
 95 100 105  
 Arg Cys Thr Gly Asp Asn Glu Lys Val Lys Ala His Ile Leu Leu  
 110 115 120  
 Thr Ala Gly Ile Ile Phe Ile Ile Thr Gly Met Val Val Leu Ile  
 125 130 135  
 Pro Val Ser Trp Val Ala Asn Ala Ile Ile Arg Asp Phe Tyr Asn  
 140 145 150  
 Ser Ile Val Asn Val Ala Gln Lys Arg Glu Leu Gly Glu Ala Leu  
 155 160 165  
 Tyr Leu Gly Trp Thr Thr Ala Leu Val Leu Ile Val Gly Gly Ala  
 170 175 180  
 Leu Phe Cys Cys Val Phe Cys Cys Asn Glu Lys Ser Ser Ser Tyr  
 185 190 195  
 Arg Tyr Ser Ile Pro Ser His Arg Thr Thr Gln Lys Ser Tyr His  
 200 205 210



Thr	Gly	Lys	Lys	Ser	Pro	Ser	Val	Tyr	Ser	Arg	Ser	Gln	Tyr	Val
				215				220						225

<210> 329  
 <211> 1315  
 <212> DNA  
 <213> Homo sapiens

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 gaccgctttc atcggaaca gcatcgtggt ggcccagggt gtgtgggagg 150  
 gcctgtggat gtctgcgtg gtgcagagca ccggccagat gcagtgaag 200  
 gtgtacgact cactgctggc gctgccacag gacctgcagg ctgcacgtgc 250  
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 ttgctggggc caagtgtacc acctgtgtgg aggagaagga ttccaaggcc 350  
 cgctgtgtgc tcacctctgg gattgtcttt gtcattctag gggctctgac 400  
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 ttgggctggg cggcctcagg cttttgttg ctgggtgggg ggttgctgtg 550  
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 accaagaatt acgtctgacg tggaggggaa tgggggctcc gctggcgcta 700  
 gagccatcca gaagtggcag tgcccaacag ctttgggatg ggttcgtacc 750  
 ttttgtttct gcctcctgct atttttcttt tgactgagga tatttaaaat 800  
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 gctgtttctc acccttgat gatggagcca aagaggggat gctttgagat 900  
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 aaaaacaaat catctgttaa caaaggactg cccacctccg gaacttctga 1150  
 cctctgtttc ctccgtctg ataagacgtc cccccccag ggccagggtcc 1200  
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tgttttgtta gtgca 1315

<210> 330

<211> 220

<212> PRT

<213> Homo sapiens

<400> 330

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Leu	Gly	Trp	Val	Asn	Gly	Leu	Val	Ser	Cys	Ala	Leu	Pro	Met	Trp
			20						25					30

Lys	Val	Thr	Ala	Phe	Ile	Gly	Asn	Ser	Ile	Val	Val	Ala	Gln	Val
				35					40					45

Val	Trp	Glu	Gly	Leu	Trp	Met	Ser	Cys	Val	Val	Gln	Ser	Thr	Gly
				50					55					60

Gln	Met	Gln	Cys	Lys	Val	Tyr	Asp	Ser	Leu	Leu	Ala	Leu	Pro	Gln
				65					70					75

Asp	Leu	Gln	Ala	Ala	Arg	Ala	Leu	Cys	Val	Ile	Ala	Leu	Leu	Val
				80					85					90

Ala	Leu	Phe	Gly	Leu	Leu	Val	Tyr	Leu	Ala	Gly	Ala	Lys	Cys	Thr
				95					100					105

Thr	Cys	Val	Glu	Glu	Lys	Asp	Ser	Lys	Ala	Arg	Leu	Val	Leu	Thr
				110					115					120

Ser	Gly	Ile	Val	Phe	Val	Ile	Ser	Gly	Val	Leu	Thr	Leu	Ile	Pro
				125					130					135

Val	Cys	Trp	Thr	Ala	His	Ala	Ile	Ile	Arg	Asp	Phe	Tyr	Asn	Pro
				140					145					150

Leu	Val	Ala	Glu	Ala	Gln	Lys	Arg	Glu	Leu	Gly	Ala	Ser	Leu	Tyr
				155					160					165

Leu	Gly	Trp	Ala	Ala	Ser	Gly	Leu	Leu	Leu	Leu	Gly	Gly	Gly	Leu
				170					175					180

Leu	Cys	Cys	Thr	Cys	Pro	Ser	Gly	Gly	Ser	Gln	Gly	Pro	Ser	His
				185					190					195

Tyr	Met	Ala	Arg	Tyr	Ser	Thr	Ser	Ala	Pro	Ala	Ile	Ser	Arg	Gly
				200					205					210

Pro	Ser	Glu	Tyr	Pro	Thr	Lys	Asn	Tyr	Val
				215					220

<210> 331

<211> 1160

<212> DNA

<213> Homo sapiens

<400> 331

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gttccttggc atggtgggga ctcttgccac aacccttctg cctcagtgg 200  
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ggaagggctc tggatgaatt gcatccgaca agccagggtc cggttgcaat 300  
gcaagttcta tagctccttg ttggctctcc cgcctgcctt ggaaacagcc 350  
cgggccctca tgtgtgtggc tgttgctctc tccttgatcg ccctgcttat 400  
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ccaaagcata cttcttggga acttcaggag tcctcttcat cctgacgggt 500  
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tttctacaac ccagccatcc acataggtca gaaacgagag ctgggagcag 600  
cacttttcct tggctgggca agcgtgctg tcctcttcat tggaggggg 650  
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ccaagtatgg actatgggtc atgtttttta taaagtcctg ctagaaactg 850  
taagtatgtg aggcaggaga acttgcttta tgtctagatt tacattgata 900  
cgaaagtttc aatttggtac tgggtggtagg aatgaaaatg acttacttgg 950  
acattctgac ttcaggtgta ttaaatacat tgactattgt tggaccaat 1000  
cgctgctcca attttcatat tctaaattca agtataacca taatcattag 1050  
caagtgtaca atgatggact acttattact ttttgacct catgtattat 1100  
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<210> 332

<211> 173

<212> PRT

<213> Homo sapiens

<400> 332

Met Asn Cys Ile Arg Gln Ala Arg Val Arg Leu Gln Cys Lys Phe

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	20	25	30
Ala Leu Met Cys Val	Ala Val Ala Leu Ser Leu Ile Ala Leu Leu		
	35	40	45
Ile Gly Ile Cys Gly	Met Lys Gln Val Gln Cys Thr Gly Ser Asn		
	50	55	60
Glu Arg Ala Lys Ala	Tyr Leu Leu Gly Thr Ser Gly Val Leu Phe		
	65	70	75
Ile Leu Thr Gly Ile	Phe Val Leu Ile Pro Val Ser Trp Thr Ala		
	80	85	90
Asn Ile Ile Ile Arg	Asp Phe Tyr Asn Pro Ala Ile His Ile Gly		
	95	100	105
Gln Lys Arg Glu Leu	Gly Ala Ala Leu Phe Leu Gly Trp Ala Ser		
	110	115	120
Ala Ala Val Leu Phe	Ile Gly Gly Gly Leu Leu Cys Gly Phe Cys		
	125	130	135
Cys Cys Asn Arg Lys	Lys Gln Gly Tyr Arg Tyr Pro Val Pro Gly		
	140	145	150
Tyr Arg Val Pro His	Thr Asp Lys Arg Arg Asn Thr Thr Met Leu		
	155	160	165
Ser Lys Thr Ser Thr	Ser Tyr Val		
	170		

<210> 333  
 <211> 535  
 <212> DNA  
 <213> Homo sapiens

<400> 333  
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 ctccagaagct gctagtctgt ctccaaaaaa agtggactgc agcatttaca 150  
 agaagtatcc agtgggtggcc atcccctgcc ccatcacata cctaccagtt 200  
 tgtggttctg actacatcac ctatgggaat gaatgtcact tgtgtaccga 250  
 gagcttgaaa agtaatggaa gagttcagtt tcttcacgat ggaagttgct 300  
 aaattctcca tggacataga gagaaaggaa tgatattctc atcatcatct 350  
 tcatcatccc aggcctctgac tgagtttctt tcagttttac tgatgttctg 400  
 ggtggggggac agagccagat tcagagtaat ctgactgaa tggagaaagt 450

ttctgtgcta cccctacaaa cccatgcctc actgacagac cagcattttt 500

tttttaacac gtcaataaaa aaataatctc ccaga 535

<210> 334

<211> 85

<212> PRT

<213> Homo sapiens

<400> 334

Met Lys Ile Thr Gly Gly Leu Leu Leu Leu Cys Thr Val Val Tyr  
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Phe Cys Ser Ser Ser Glu Ala Ala Ser Leu Ser Pro Lys Lys Val  
20 25 30

Asp Cys Ser Ile Tyr Lys Lys Tyr Pro Val Val Ala Ile Pro Cys  
35 40 45

Pro Ile Thr Tyr Leu Pro Val Cys Gly Ser Asp Tyr Ile Thr Tyr  
50 55 60

Gly Asn Glu Cys His Leu Cys Thr Glu Ser Leu Lys Ser Asn Gly  
65 70 75

Arg Val Gln Phe Leu His Asp Gly Ser Cys  
80 85

<210> 335

<211> 742

<212> DNA

<213> Homo sapiens

<400> 335

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ggcataagtg gaaataaact caagctgatg cttcaaaaac gagaagcacc 200

tgttccaact aagactaaag tggccgttga tgagaataaa gccaaagaat 250

tccttggcag cctgaagcgc cagaagcggc agctgtggga ccggactcgg 300

cccagggtgc agcagtggta ccagcagttt ctctacatgg gctttgatga 350

agcgaaatth gaagatgaca tcacctattg gcttaacaga gatcgaaatg 400

gacatgaata ctatggcgat tactaccaac gtcactatga tgaagactct 450

gcaattgggtc cccggagccc ctacggcttt aggcattggag ccagcgtcaa 500

ctacgatgac tactaaccat gacttgccac acgctgtaca agaagcaa 550

agcgattctc ttcattgtatc tcctaattgcc ttacactact tggttttctga 600

tttgctctat ttcagcagat cttttctacc tactttgtgt gatcaaaaaa 650  
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cctctcattt aaaaatagaa ataaagcatt ttgttaaaaa ga 742

<210> 336  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 336  
Met Ala Ala Ser Pro Ala Arg Pro Ala Val Leu Ala Leu Thr Gly  
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Gly Asn Lys Leu Lys Leu Met Leu Gln Lys Arg Glu Ala Pro Val  
35 40 45  
Pro Thr Lys Thr Lys Val Ala Val Asp Glu Asn Lys Ala Lys Glu  
50 55 60  
Phe Leu Gly Ser Leu Lys Arg Gln Lys Arg Gln Leu Trp Asp Arg  
65 70 75  
Thr Arg Pro Glu Val Gln Gln Trp Tyr Gln Gln Phe Leu Tyr Met  
80 85 90  
Gly Phe Asp Glu Ala Lys Phe Glu Asp Asp Ile Thr Tyr Trp Leu  
95 100 105  
Asn Arg Asp Arg Asn Gly His Glu Tyr Tyr Gly Asp Tyr Tyr Gln  
110 115 120  
Arg His Tyr Asp Glu Asp Ser Ala Ile Gly Pro Arg Ser Pro Tyr  
125 130 135  
Gly Phe Arg His Gly Ala Ser Val Asn Tyr Asp Asp Tyr  
140 145

<210> 337  
<211> 1310  
<212> DNA  
<213> Homo sapiens

<400> 337  
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tgaaggggtg ggtgatgagg tgaccgtcct tttctcgggtg cttgcctgcc 150  
ttctgggtgct ggcccttgcc tgggtctcaa cgcacaccgc tgagggcggg 200  
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 aaaaaaaaa 1310

<210> 338  
 <211> 246  
 <212> PRT  
 <213> Homo sapiens

<400> 338  
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 Ser Val Leu Ala Cys Leu Leu Val Leu Ala Leu Ala Trp Val Ser  
 20 25 30  
 Thr His Thr Ala Glu Gly Gly Asp Pro Leu Pro Gln Pro Ser Gly  
 35 40 45





aggacttgga tgggtttgag gggtactccc tgagtgactg gctgtgcctg 300  
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<210> 340  
<211> 148  
<212> PRT  
<213> Homo sapiens

<400> 340  
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20 25 30  
Leu Gln Leu Glu Asp Leu Asp Gly Phe Glu Gly Tyr Ser Leu Ser  
35 40 45  
Asp Trp Leu Cys Leu Ala Phe Val Glu Ser Lys Phe Asn Ile Ser  
50 55 60  
Lys Ile Asn Glu Asn Ala Asp Gly Ser Phe Asp Tyr Gly Leu Phe  
65 70 75  
Gln Ile Asn Ser His Tyr Trp Cys Asn Asp Tyr Lys Ser Tyr Ser  
80 85 90  
Glu Asn Leu Cys His Val Asp Cys Gln Asp Leu Leu Asn Pro Asn  
95 100 105  
Leu Leu Ala Gly Ile His Cys Ala Lys Arg Ile Val Ser Gly Ala  
110 115 120  
Arg Gly Met Asn Asn Trp Val Glu Trp Arg Leu His Cys Ser Gly  
125 130 135  
Arg Pro Leu Ser Tyr Trp Leu Thr Gly Cys Arg Leu Arg

<210> 341  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 341  
 ccctccaagg atgacaaagg cgc 23

<210> 342  
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 <212> DNA  
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<220>  
 <221> Artificial Sequence  
 <222> 1-29  
 <223> Synthetic construct.

<400> 342  
 ggtcagcagc tttcttgccc taaatcagg 29

<210> 343  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 343  
 atctcaggcg gcatcctgtc agcc 24

<210> 344  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 344  
 gtggatgcct gcaagaaggt tggg 24

<210> 345  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-45  
<223> Synthetic construct.

<400> 345  
agcttttcttg ccctaaatca ggccagcctc atcagtcgct gtgac 45

<210> 346  
<211> 2575  
<212> DNA  
<213> Homo sapiens

<400> 346  
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aaggagaaaa ccggggtaaa gggaggggaag caattcaatt tgaagtccct 200  
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<210> 347

<211> 639

<212> PRT

<213> Homo sapiens

<400> 347

Met	Leu	Leu	Arg	Lys	Arg	Tyr	Arg	His	Arg	Pro	Cys	Arg	Leu	Gln
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Phe	Leu	Leu	Leu	Leu	Leu	Met	Leu	Gly	Cys	Val	Leu	Met	Met	Val
				20					25					30

Ala	Met	Leu	His	Pro	Pro	His	His	Thr	Leu	His	Gln	Thr	Val	Thr
				35					40					45

Ala	Gln	Ala	Ser	Lys	His	Ser	Pro	Glu	Ala	Arg	Tyr	Arg	Leu	Asp
				50					55					60

Phe	Gly	Glu	Ser	Gln	Asp	Trp	Val	Leu	Glu	Ala	Glu	Asp	Glu	Gly
				65					70					75

Glu	Glu	Tyr	Ser	Pro	Leu	Glu	Gly	Leu	Pro	Pro	Phe	Ile	Ser	Leu
				80					85					90

Arg	Glu	Asp	Gln	Leu	Leu	Val	Ala	Val	Ala	Leu	Pro	Gln	Ala	Arg
				95					100					105

Arg	Asn	Gln	Ser	Gln	Gly	Arg	Arg	Gly	Gly	Ser	Tyr	Arg	Leu	Ile
				110					115					120

Lys	Gln	Pro	Arg	Arg	Gln	Asp	Lys	Glu	Ala	Pro	Lys	Arg	Asp	Trp
				125					130					135

Gly	Ala	Asp	Glu	Asp	Gly	Glu	Val	Ser	Glu	Glu	Glu	Glu	Leu	Thr
				140					145					150

Pro	Phe	Ser	Leu	Asp	Pro	Arg	Gly	Leu	Gln	Glu	Ala	Leu	Ser	Ala
				155					160					165

Arg	Ile	Pro	Leu	Gln	Arg	Ala	Leu	Pro	Glu	Val	Arg	His	Pro	Leu
				170					175					180

Cys	Leu	Gln	Gln	His	Pro	Gln	Asp	Ser	Leu	Pro	Thr	Ala	Ser	Val
				185					190					195

Ile	Leu	Cys	Phe	His	Asp	Glu	Ala	Trp	Ser	Thr	Leu	Leu	Arg	Thr
				200					205					210

Val	His	Ser	Ile	Leu	Asp	Thr	Val	Pro	Arg	Ala	Phe	Leu	Lys	Glu
				215					220					225

Ile	Ile	Leu	Val	Asp	Asp	Leu	Ser	Gln	Gln	Gly	Gln	Leu	Lys	Ser
				230					235					240

Ala	Leu	Ser	Glu	Tyr	Val	Ala	Arg	Leu	Glu	Gly	Val	Lys	Leu	Leu
				245					250					255

Arg Ser Asn Lys	Arg Leu Gly Ala Ile	Arg Ala Arg Met Leu Gly	260	265	270
Ala Thr Arg Ala	Thr Gly Asp Val Leu	Val Phe Met Asp Ala His	275	280	285
Cys Glu Cys His	Pro Gly Trp Leu Glu	Pro Leu Leu Ser Arg Ile	290	295	300
Ala Gly Asp Arg	Ser Arg Val Val Ser	Pro Val Ile Asp Val Ile	305	310	315
Asp Trp Lys Thr	Phe Gln Tyr Tyr Pro	Ser Lys Asp Leu Gln Arg	320	325	330
Gly Val Leu Asp	Trp Lys Leu Asp Phe	His Trp Glu Pro Leu Pro	335	340	345
Glu His Val Arg	Lys Ala Leu Gln Ser	Pro Ile Ser Pro Ile Arg	350	355	360
Ser Pro Val Val	Pro Gly Glu Val Val	Ala Met Asp Arg His Tyr	365	370	375
Phe Gln Asn Thr	Gly Ala Tyr Asp Ser	Leu Met Ser Leu Arg Gly	380	385	390
Gly Glu Asn Leu	Glu Leu Ser Phe Lys	Ala Trp Leu Cys Gly Gly	395	400	405
Ser Val Glu Ile	Leu Pro Cys Ser Arg	Val Gly His Ile Tyr Gln	410	415	420
Asn Gln Asp Ser	His Ser Pro Leu Asp	Gln Glu Ala Thr Leu Arg	425	430	435
Asn Arg Val Arg	Ile Ala Glu Thr Trp	Leu Gly Ser Phe Lys Glu	440	445	450
Thr Phe Tyr Lys	His Ser Pro Glu Ala	Phe Ser Leu Ser Lys Ala	455	460	465
Glu Lys Pro Asp	Cys Met Glu Arg Leu	Gln Leu Gln Arg Arg Leu	470	475	480
Gly Cys Arg Thr	Phe His Trp Phe Leu	Ala Asn Val Tyr Pro Glu	485	490	495
Leu Tyr Pro Ser	Glu Pro Arg Pro Ser	Phe Ser Gly Lys Leu His	500	505	510
Asn Thr Gly Leu	Gly Leu Cys Ala Asp	Cys Gln Ala Glu Gly Asp	515	520	525
Ile Leu Gly Cys	Pro Met Val Leu Ala	Pro Cys Ser Asp Ser Arg	530	535	540
Gln Gln Gln Tyr	Leu Gln His Thr Ser	Arg Lys Glu Ile His Phe			

	545		550		555
Gly Ser Pro Gln	His Leu Cys Phe Ala	Val Arg Gln Glu Gln	Val		
	560		565		570
Ile Leu Gln Asn	Cys Thr Glu Glu Gly	Leu Ala Ile His Gln	Gln		
	575		580		585
His Trp Asp Phe	Gln Glu Asn Gly Met	Ile Val His Ile Leu	Ser		
	590		595		600
Gly Lys Cys Met	Glu Ala Val Val Gln	Glu Asn Asn Lys Asp	Leu		
	605		610		615
Tyr Leu Arg Pro	Cys Asp Gly Lys Ala	Arg Gln Gln Trp Arg	Phe		
	620		625		630
Asp Gln Ile Asn	Ala Val Asp Glu Arg				
	635				

<210> 348  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 348  
 ggagaggtgg tggccatgga cag 23

<210> 349  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 349  
 ctgtcactgc aaggagccaa cacc 24

<210> 350  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 350  
 tatgtcgctg cgaggtggtg aaaacctcga actgtctttc aaggc 45

<210> 351  
 <211> 2524  
 <212> DNA  
 <213> Homo sapiens

<400> 351  
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<210> 352

<211> 243

<212> PRT

<213> Homo sapiens

<400> 352

Met	Arg	Pro	Gln	Gly	Pro	Ala	Ala	Ser	Pro	Gln	Arg	Leu	Arg	Gly
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 20 25 30  
 Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
 35 40 45  
 Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
 50 55 60  
 Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
 65 70 75  
 Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
 80 85 90  
 Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
 95 100 105  
 Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
 110 115 120  
 Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
 125 130 135  
 Ala Leu Arg Val Leu Phe Ser Gly Ser Leu Arg Leu Lys Cys Arg  
 140 145 150  
 Asn Ala Cys Cys Gln Arg Trp Tyr Phe Thr Phe Asn Gly Ala Glu  
 155 160 165  
 Cys Ser Gly Pro Leu Pro Ile Glu Ala Ile Ile Tyr Leu Asp Gln  
 170 175 180  
 Gly Ser Pro Glu Met Asn Ser Thr Ile Asn Ile His Arg Thr Ser  
 185 190 195  
 Ser Val Glu Gly Leu Cys Glu Gly Ile Gly Ala Gly Leu Val Asp  
 200 205 210  
 Val Ala Ile Trp Val Gly Thr Cys Ser Asp Tyr Pro Lys Gly Asp  
 215 220 225  
 Ala Ser Thr Gly Trp Asn Ser Val Ser Arg Ile Ile Ile Glu Glu  
 230 235 240

Leu Pro Lys

<210> 353

<211> 480

<212> DNA

<213> Homo sapiens

<400> 353

gttaaccagc gcagtcctcc gtgcgtcccg cccgccgctg cctcactcc 50

cggccaggat ggcacctgt ctggccctgc gcatggcgct gctgctggtc 100

tccgggggttc tggccctgc ggtgctcaca gacgatgttc cacaggagcc 150  
 cgtgcccacg ctgtggaacg agccggccga gctgccgtcg ggagaaggcc 200  
 ccgtggagag caccagcccc ggccgggagc ccgtggacac cggccccca 250  
 gccccaccg tcgcgccagg acccgaggac agcaccgcgc aggagcggct 300  
 ggaccagggc ggcgggtcgc tggggcccg cgctatcgcg gccatcgtga 350  
 tcgccgcct gctggccacc tgcgtggtgc tggcgctcgt ggtcgtcgcg 400  
 ctgagaaagt ttctgcctc ctgaagcgaa taaaggggcc gcgccggcc 450  
 gcggcgcgac tcggcaaaaa aaaaaaaaaa 480

<210> 354  
 <211> 121  
 <212> PRT  
 <213> Homo sapiens

<400> 354  
 Met Ala Ser Cys Leu Ala Leu Arg Met Ala Leu Leu Leu Val Ser  
 1 5 10 15  
 Gly Val Leu Ala Pro Ala Val Leu Thr Asp Asp Val Pro Gln Glu  
 20 25 30  
 Pro Val Pro Thr Leu Trp Asn Glu Pro Ala Glu Leu Pro Ser Gly  
 35 40 45  
 Glu Gly Pro Val Glu Ser Thr Ser Pro Gly Arg Glu Pro Val Asp  
 50 55 60  
 Thr Gly Pro Pro Ala Pro Thr Val Ala Pro Gly Pro Glu Asp Ser  
 65 70 75  
 Thr Ala Gln Glu Arg Leu Asp Gln Gly Gly Gly Ser Leu Gly Pro  
 80 85 90  
 Gly Ala Ile Ala Ala Ile Val Ile Ala Ala Leu Leu Ala Thr Cys  
 95 100 105  
 Val Val Leu Ala Leu Val Val Val Ala Leu Arg Lys Phe Ser Ala  
 110 115 120

Ser

<210> 355  
 <211> 2134  
 <212> DNA  
 <213> Homo sapiens

<400> 355  
 ggccgttggt tgggtgcgcg ctgaagggtg tggcgcgagc agcgtcgttg 50  
 gttggccggc ggcggggccg gacgggcatg gccctgctgc tgtgcctggt 100



cctgggacac acagagccac cccggccttg tgagtgaccc agagaaggga 1600  
 ggcctcggga gaaggggtgc tcgtaagcca acaccagcgt gccgcggcct 1650  
 gcacaccctt cggacatccc aggcacgagg gtgtcgtgga tgtggccaca 1700  
 cataggacca cacgtcccag ctgggaggag aggcctgggg cccccaggga 1750  
 gggaggcagg ggggtggggga catggagagc tgaggcagcc tcgtctcccc 1800  
 gcagcctggt atcgccagcc ttaaggtgtc tggagcccc acacttggcc 1850  
 aacctgacct tggaagatgc tgctgagtgt ctcaagcagc actgacagca 1900  
 gctgggcctg ccccagggca acgtgggggc ggagactcag ctggacagcc 1950  
 cctgcctgtc actctggagc tgggctgctg ctgcctcagg accccctctc 2000  
 cgaccccgga cagagctgag ctggccaggg ccaggagggc gggagggagg 2050  
 gaatgggggt gggctgtgcg cagcatcagc gcctgggcag gtccgcagag 2100  
 ctgcgggatg tgattaaagt ccctgatgtt tctc 2134

<210> 356  
 <211> 157  
 <212> PRT  
 <213> Homo sapiens

<400> 356  
 Met Ala Leu Leu Leu Cys Leu Val Cys Leu Thr Ala Ala Leu Ala  
 1 5 10 15  
 His Gly Cys Leu His Cys His Ser Asn Phe Ser Lys Lys Phe Ser  
 20 25 30  
 Phe Tyr Arg His His Val Asn Phe Lys Ser Trp Trp Val Gly Asp  
 35 40 45  
 Ile Pro Val Ser Gly Ala Leu Leu Thr Asp Trp Ser Asp Asp Thr  
 50 55 60  
 Met Lys Glu Leu His Leu Ala Ile Pro Ala Lys Ile Thr Arg Glu  
 65 70 75  
 Lys Leu Asp Gln Val Ala Thr Ala Val Tyr Gln Met Met Asp Gln  
 80 85 90  
 Leu Tyr Gln Gly Lys Met Tyr Phe Pro Gly Tyr Phe Pro Asn Glu  
 95 100 105  
 Leu Arg Asn Ile Phe Arg Glu Gln Val His Leu Ile Gln Asn Ala  
 110 115 120  
 Ile Ile Glu Arg His Leu Ala Pro Gly Ser Trp Gly Gly Gly Gln  
 125 130 135  
 Leu Ser Arg Glu Gly Pro Ser Leu Ala Pro Glu Gly Ser Met Pro

140

145

150

Ser Pro Arg Gly Asp Leu Pro  
155

&lt;210&gt; 357

&lt;211&gt; 1536

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;400&gt; 357

agcaggagca ggagagggac aatggaagct gccccgtcca ggttcatgtt 50  
cctcttattt ctctcacgt gtgagctggc tgcagaagtt gctgcagaag 100  
ttgagaaatc ctcagatggc cctgggtgctg cccaggaacc cacgtggctc 150  
acagatgtcc cagctgccat ggaattcatt gctgccactg aggtggctgt 200  
cataggcttc ttccaggatt tagaaatacc agcagtgcc atactccata 250  
gcatggtgca aaaattccca ggcgtgtcat ttgggatcag cactgattct 300  
gaggttctga cacactacaa catcactggg aacaccatct gcctctttcg 350  
cctggtagac aatgaacaac tgaatttaga ggacgaagac attgaaagca 400  
ttgatgccac caaattgagc cgtttcattg agatcaacag cctccacatg 450  
gtgacagagt acaaccctgt gactgtgatt gggttattca acagcgtaat 500  
tcagattcat ctctctctga taatgaacaa ggcctcccca gagtatgaag 550  
agaacatgca cagataccag aaggcagcca agctcttcca ggggaagatt 600  
ctctttattc tgggtggacag tggatatgaaa gaaaatggga aggtgatatc 650  
atttttcaaa cttaaaggagt ctcaactgcc agctttggca atttaccaga 700  
ctctagatga cgagtgggat aactgcccc cagcagaagt ttccgtagag 750  
catgtgcaaa acttttgtga tggattccta agtggaaaat tgttgaaaga 800  
aaatcgtgaa tcagaaggaa agactccaaa ggtggaactc tgacttctcc 850  
ttggaactac atatggccaa gtatctactt tatgcaaagt aaaaaggcac 900  
aactcaaatc tcagagacac taaacaacag gatcactagg cctgccaacc 950  
acacacacac gcacgtgcac acacgcacgc acgcgtgcac acacacacgc 1000  
gcacacacac acacacacag agcttcattt cctgtcttaa aatctcgttt 1050  
tctcttcttc cttcttttaa atttcatatc ctactccct atccaatttc 1100  
cttcttatcg tgcattcata ctctgtaagc ccatctgtaa cacacctaga 1150  
tcaaggcttt aagagactca ctgtgatgcc tctatgaaag agaggcattc 1200

ctagagaaag attgttccaa tttgtcattt aatatcaagt ttgtatactg 1250  
cacatgactt acacacaaca tagttcctgc tcttttaagg ttacctaagg 1300  
gttgaaactc taccttcttt cataagcaca tgtccgtctc tgactcagga 1350  
tcaaaaacca aaggatggtt ttaaacacct ttgtgaaatt gtctttttgc 1400  
cagaagttaa aggctgtctc caagtccttg aactcagcag aaatagacca 1450  
tgtgaaaact ccatgcttgg ttagcatctc caactcccta tgtaaataca 1500  
caacctgcat aataaataaa aggcaatcat gttata 1536

<210> 358  
<211> 273  
<212> PRT  
<213> Homo sapiens

<400> 358  
Met Glu Ala Ala Pro Ser Arg Phe Met Phe Leu Leu Phe Leu Leu  
1 5 10 15  
Thr Cys Glu Leu Ala Ala Glu Val Ala Ala Glu Val Glu Lys Ser  
20 25 30  
Ser Asp Gly Pro Gly Ala Ala Gln Glu Pro Thr Trp Leu Thr Asp  
35 40 45  
Val Pro Ala Ala Met Glu Phe Ile Ala Ala Thr Glu Val Ala Val  
50 55 60  
Ile Gly Phe Phe Gln Asp Leu Glu Ile Pro Ala Val Pro Ile Leu  
65 70 75  
His Ser Met Val Gln Lys Phe Pro Gly Val Ser Phe Gly Ile Ser  
80 85 90  
Thr Asp Ser Glu Val Leu Thr His Tyr Asn Ile Thr Gly Asn Thr  
95 100 105  
Ile Cys Leu Phe Arg Leu Val Asp Asn Glu Gln Leu Asn Leu Glu  
110 115 120  
Asp Glu Asp Ile Glu Ser Ile Asp Ala Thr Lys Leu Ser Arg Phe  
125 130 135  
Ile Glu Ile Asn Ser Leu His Met Val Thr Glu Tyr Asn Pro Val  
140 145 150  
Thr Val Ile Gly Leu Phe Asn Ser Val Ile Gln Ile His Leu Leu  
155 160 165  
Leu Ile Met Asn Lys Ala Ser Pro Glu Tyr Glu Glu Asn Met His  
170 175 180  
Arg Tyr Gln Lys Ala Ala Lys Leu Phe Gln Gly Lys Ile Leu Phe  
185 190 195

Ile	Leu	Val	Asp	Ser	Gly	Met	Lys	Glu	Asn	Gly	Lys	Val	Ile	Ser	
				200					205					210	
Phe	Phe	Lys	Leu	Lys	Glu	Ser	Gln	Leu	Pro	Ala	Leu	Ala	Ile	Tyr	
				215					220					225	
Gln	Thr	Leu	Asp	Asp	Glu	Trp	Asp	Thr	Leu	Pro	Thr	Ala	Glu	Val	
				230					235					240	
Ser	Val	Glu	His	Val	Gln	Asn	Phe	Cys	Asp	Gly	Phe	Leu	Ser	Gly	
				245					250					255	
Lys	Leu	Leu	Lys	Glu	Asn	Arg	Glu	Ser	Glu	Gly	Lys	Thr	Pro	Lys	
				260					265					270	

Val Glu Leu

<210> 359  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 359  
 ccagcagtgc ccatactcca tagc 24

<210> 360  
 <211> 20  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-20  
 <223> Synthetic construct.

<400> 360  
 tgacgagtgg gatacactgc 20

<210> 361  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 361  
 gctctacgga aacttctgct gtgg 24

<210> 362



<211> 50  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-50  
<223> Synthetic construct.

<400> 362  
attcccaggc gtgtcatttg ggatcagcac tgattctgag gttctgacac 50

<210> 363  
<211> 1777  
<212> DNA  
<213> Homo sapiens

<400> 363  
ggagagccgc ggctgggacc ggagtgggga gcgcggcgtg gaggtgccac 50  
ccggcgcggg tggcgagag atcagaagcc tcttcccaa gccgagccaa 100  
cctcagcggg gaccgggct caggacgcg gcggcgcgcg cggcgactgc 150  
agtggctgga cgatggcagc gtccgccgga gccggggcgg tgattgcagc 200  
cccagacagc cggcgctggc tgtggtcggg gctggcgcg gcgcttgggc 250  
tcttgacagc tggagtatca gccttgaag tatatacgcc aaaagaaatc 300  
ttcgtggcaa atggtacaca agggaagctg acctgcaagt tcaagtctac 350  
tagtacgact ggcgggttga cctcagctc ctggagcttc cagccagagg 400  
gggccgacac tactgtgtcg tttttccact actcccaagg gcaagtgtac 450  
cttgggaatt atccaccatt taaagacaga atcagctggg ctggagacct 500  
tgacaagaaa gatgcatcaa tcaacataga aaatatgcag ttatacaca 550  
atggcaccta tatctgtgat gtcaaaaacc ctctgacat cgttgtccag 600  
cctggacaca ttaggctcta tgtcgtagaa aaagagaatt tgctgtgtt 650  
tccagtttgg gtagtggtgg gcatagttac tgctgtggc ctaggtctca 700  
ctctgctcat cagcatgatt ctggctgtcc tctatagaag gaaaaactct 750  
aaacgggatt aactggctg cagtacatca gagagtttgt caccagttaa 800  
gcaggctcct cggaagtccc cctccgacac tgagggtcct gtaaagagtc 850  
tgcttcttgg atctcaccag ggcccagtca tatatgcaca gttagaccac 900  
tccggcgga atcacagtga caagattaac aagtcagagt ctgtggtgta 950  
tgcggatatc cgaaagaatt aagagaatac ctagaacata tctcagcaa 1000

gaaacaaaac caaactggac tctcgtgcag aaaatgtagc ccattaccac 1050  
atgtagcctt ggagaccag gcaaggacaa gtacacgtgt actcacagag 1100  
ggagagaaag atgtgtacaa aggatatgta taaatattct atttagtcat 1150  
cctgatatga ggagccagtg ttgcatgatg aaaagatggt atgattctac 1200  
atatgtaccc attgtcttgc tgtttttgta ctttcttttc aggtcattta 1250  
caattgggag atttcagaaa cattcctttc accatcattt agaaatgggt 1300  
tgccttaatg gagacaatag cagatcctgt agtatttcca gtagacatgg 1350  
ccttttaatc taagggctta agactgatta gtcttagcat ttactgtagt 1400  
tggaggatgg agatgctatg atggaagcat acccaggggtg gccttttagca 1450  
cagtatcagt accattttatt tgtctgccgc ttttaaaaaa taccatttgg 1500  
ctatgccact tgaaaacaat ttgagaagtt tttttgaagt ttttctcact 1550  
aaaatatggg gcaattgtta gccttacatg ttgtgtagac ttactttaag 1600  
tttgcaacct tgaaatgtgt catatcaatt tctggattca taatagcaag 1650  
attagcaaag gataaatgcc gaaggtcact tcattctgga cacagttgga 1700  
tcaatactga ttaagtagaa aatccaagct ttgcttgaga acttttgtaa 1750  
cgtggagagt aaaaagtatc ggtttta 1777

<210> 364  
<211> 269  
<212> PRT  
<213> Homo sapiens

<400> 364  
Met Ala Ala Ser Ala Gly Ala Gly Ala Val Ile Ala Ala Pro Asp  
1 5 10 15  
Ser Arg Arg Trp Leu Trp Ser Val Leu Ala Ala Ala Leu Gly Leu  
20 25 30  
Leu Thr Ala Gly Val Ser Ala Leu Glu Val Tyr Thr Pro Lys Glu  
35 40 45  
Ile Phe Val Ala Asn Gly Thr Gln Gly Lys Leu Thr Cys Lys Phe  
50 55 60  
Lys Ser Thr Ser Thr Thr Gly Gly Leu Thr Ser Val Ser Trp Ser  
65 70 75  
Phe Gln Pro Glu Gly Ala Asp Thr Thr Val Ser Phe Phe His Tyr  
80 85 90  
Ser Gln Gly Gln Val Tyr Leu Gly Asn Tyr Pro Pro Phe Lys Asp  
95 100 105

Arg	Ile	Ser	Trp	Ala	Gly	Asp	Leu	Asp	Lys	Lys	Asp	Ala	Ser	Ile
				110					115					120
Asn	Ile	Glu	Asn	Met	Gln	Phe	Ile	His	Asn	Gly	Thr	Tyr	Ile	Cys
				125					130					135
Asp	Val	Lys	Asn	Pro	Pro	Asp	Ile	Val	Val	Gln	Pro	Gly	His	Ile
				140					145					150
Arg	Leu	Tyr	Val	Val	Glu	Lys	Glu	Asn	Leu	Pro	Val	Phe	Pro	Val
				155					160					165
Trp	Val	Val	Val	Gly	Ile	Val	Thr	Ala	Val	Val	Leu	Gly	Leu	Thr
				170					175					180
Leu	Leu	Ile	Ser	Met	Ile	Leu	Ala	Val	Leu	Tyr	Arg	Arg	Lys	Asn
				185					190					195
Ser	Lys	Arg	Asp	Tyr	Thr	Gly	Cys	Ser	Thr	Ser	Glu	Ser	Leu	Ser
				200					205					210
Pro	Val	Lys	Gln	Ala	Pro	Arg	Lys	Ser	Pro	Ser	Asp	Thr	Glu	Gly
				215					220					225
Leu	Val	Lys	Ser	Leu	Pro	Ser	Gly	Ser	His	Gln	Gly	Pro	Val	Ile
				230					235					240
Tyr	Ala	Gln	Leu	Asp	His	Ser	Gly	Gly	His	His	Ser	Asp	Lys	Ile
				245					250					255
Asn	Lys	Ser	Glu	Ser	Val	Val	Tyr	Ala	Asp	Ile	Arg	Lys	Asn	
				260					265					

<210> 365  
 <211> 1321  
 <212> DNA  
 <213> Homo sapiens

<400> 365  
 gccggctgtg cagagacgcc atgtaccggc tcctgtcagc agtgactgcc 50  
 cgggctgccg cccccggggg cttggcctca agctgcggac gacgcggggt 100  
 ccatcagcgc gccgggctgc cgctctcgg ccacggctgg gtcggggggc 150  
 tcgggctggg gctggggctg gcgctcgggg tgaagctggc aggtgggctg 200  
 aggggcgcg ccccgggcga gtcccccgcg gccccgacc ctgaggcgctc 250  
 gcctctggcc gagccgccac aggagcagtc cctcgccccg tggctctccg 300  
 agaccccggc gccgccctgc tccaggtgct tcgccagagc catcgagagc 350  
 agccgcgacc tgctgcacag gatcaaggat gaggtgggcg caccgggcat 400  
 agtggttgga gtttctgtag atggaaaaga agtctggtca gaaggtttag 450  
 gttatgctga tgttgagaac cgtgtaccat gtaaaccaga gacagttatg 500

cgaattgcta gcatcagcaa aagtctcacc atggttgctc ttgccaaatt 550  
 gtgggaagca gggaaactgg atcttgatat tccagtacaa cattatgttc 600  
 ccgaattccc agaaaaagaa tatgaagggtg aaaagggttc tgtcacaaca 650  
 agattactga tttcccatTT aagtggaatt cgtcattatg aaaaggacat 700  
 aaaaaagggtg aaagaagaga aagcttataa agccttgaag atgatgaaag 750  
 agaatgttgc atttgagcaa gaaaaagaag gcaaaagtaa tgaaaagaat 800  
 gattttacta aattttaaac agagcaggag aatgaagcca aatgccggaa 850  
 ttcaaaacct ggcaagaaaa agaattgattt tgaacaaggc gaattatatt 900  
 tgagagaaaa gtttgaaaat tcaattgaat ccctaagatt atttaaaaat 950  
 gatcctttgt tcttcaaacc tggtagtcag tttttgtatt caacttttgg 1000  
 ctatacccta ctggcagcca tagtagagag agcttcagga tgtaaattatt 1050  
 tggactatat gcagaaaata ttccatgact tggatatgct gacgactgtg 1100  
 caggaagaaa acgagccagt gatttacaat agagcaaggT aaatgaatac 1150  
 cttctgctgt gtctagctat atcgcatctt aacactattt tattaattaa 1200  
 aagtcaaatt ttctttgttt ccattccaaa atcaacctgc cacattttgg 1250  
 gagcttttct acatgtctgt tttctcatct gtaaagtgaa ggaagtaaaa 1300  
 catgtttata aagtaaaaaa a 1321

<210> 366  
 <211> 373  
 <212> PRT  
 <213> Homo sapiens

<400> 366  
 Met Tyr Arg Leu Leu Ser Ala Val Thr Ala Arg Ala Ala Ala Pro  
 1 5 10 15  
 Gly Gly Leu Ala Ser Ser Cys Gly Arg Arg Gly Val His Gln Arg  
 20 25 30  
 Ala Gly Leu Pro Pro Leu Gly His Gly Trp Val Gly Gly Leu Gly  
 35 40 45  
 Leu Gly Leu Gly Leu Ala Leu Gly Val Lys Leu Ala Gly Gly Leu  
 50 55 60  
 Arg Gly Ala Ala Pro Ala Gln Ser Pro Ala Ala Pro Asp Pro Glu  
 65 70 75  
 Ala Ser Pro Leu Ala Glu Pro Pro Gln Glu Gln Ser Leu Ala Pro  
 80 85 90

Trp Ser Pro Gln Thr Pro Ala Pro Pro Cys Ser Arg Cys Phe Ala	95	100		105
Arg Ala Ile Glu Ser Ser Arg Asp Leu Leu His Arg Ile Lys Asp	110	115		120
Glu Val Gly Ala Pro Gly Ile Val Val Gly Val Ser Val Asp Gly	125	130		135
Lys Glu Val Trp Ser Glu Gly Leu Gly Tyr Ala Asp Val Glu Asn	140	145		150
Arg Val Pro Cys Lys Pro Glu Thr Val Met Arg Ile Ala Ser Ile	155	160		165
Ser Lys Ser Leu Thr Met Val Ala Leu Ala Lys Leu Trp Glu Ala	170	175		180
Gly Lys Leu Asp Leu Asp Ile Pro Val Gln His Tyr Val Pro Glu	185	190		195
Phe Pro Glu Lys Glu Tyr Glu Gly Glu Lys Val Ser Val Thr Thr	200	205		210
Arg Leu Leu Ile Ser His Leu Ser Gly Ile Arg His Tyr Glu Lys	215	220		225
Asp Ile Lys Lys Val Lys Glu Glu Lys Ala Tyr Lys Ala Leu Lys	230	235		240
Met Met Lys Glu Asn Val Ala Phe Glu Gln Glu Lys Glu Gly Lys	245	250		255
Ser Asn Glu Lys Asn Asp Phe Thr Lys Phe Lys Thr Glu Gln Glu	260	265		270
Asn Glu Ala Lys Cys Arg Asn Ser Lys Pro Gly Lys Lys Lys Asn	275	280		285
Asp Phe Glu Gln Gly Glu Leu Tyr Leu Arg Glu Lys Phe Glu Asn	290	295		300
Ser Ile Glu Ser Leu Arg Leu Phe Lys Asn Asp Pro Leu Phe Phe	305	310		315
Lys Pro Gly Ser Gln Phe Leu Tyr Ser Thr Phe Gly Tyr Thr Leu	320	325		330
Leu Ala Ala Ile Val Glu Arg Ala Ser Gly Cys Lys Tyr Leu Asp	335	340		345
Tyr Met Gln Lys Ile Phe His Asp Leu Asp Met Leu Thr Thr Val	350	355		360
Gln Glu Glu Asn Glu Pro Val Ile Tyr Asn Arg Ala Arg	365	370		

&lt;210&gt; 367

<211> 30  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-30  
<223> Synthetic construct.

<400> 367  
tggaaaagaa gtctgggtcag aaggtttagg 30

<210> 368  
<211> 25  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-25  
<223> Synthetic construct.

<400> 368  
catttggtt cattctcctg ctctg 25

<210> 369  
<211> 28  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-28  
<223> Synthetic construct.

<400> 369  
aaaacctcag aacaactcat ttgacacc 28

<210> 370  
<211> 41  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-41  
<223> Synthetic construct.

<400> 370  
gtctcaccat gggtgctctt gccaaattgt gggaagcagg g 41

<210> 371  
<211> 1150  
<212> DNA  
<213> Homo sapiens

<400> 371  
gtgacactat agaagagcta tgacgtcgca tgcacgcgta cgtaagctcg 50

gaattcgggt cgaggctggt gggaagaagc cgagatggcg gcagccagcg 100  
ctggggcaac cgggctgctc ctgctcttgc tgatggcggt agcagcgccc 150  
agtcgagccc ggggcagcgg ctgccgggcc gggactggtg cgcgaggggc 200  
tggggcgga ggtcgagagg gcgaggcctg tggcacggtg gggctgctgc 250  
tggagcactc atttgagatc gatgacagt ccaacttccg gaagcggggc 300  
tcaactgctct ggaaccagca ggatggtacc ttgtccctgt cacagcgcca 350  
gctcagcgag gaggagcggg gccgactccg ggatgtggca gccctgaatg 400  
gcctgtaccg ggtccggatc ccaaggcgac ccggggccct ggatggcctg 450  
gaagctggtg gctatgtctc ctcccttctc cctgcgtgct ccctggtgga 500  
gtcgcacctg tcggaccagc tgaccctgca cgtggatgtg gccggcaacg 550  
tggtgggcgt gtcgggtggtg acgcaccccg ggggctgccg gggccatgag 600  
gtggaggacg tggacctgga gctgttcaac acctcgggtg agctgcagcc 650  
gcccaccaca gcccaggcc ctgagacggc ggccttcatt gagcgccctg 700  
agatggaaca ggcccagaag gccagaacc cccaggagca gaagtccttc 750  
ttcgccaaat actggatgta catcattccc gtcgtcctgt tcctcatgat 800  
gtcaggagcg ccagacaccg ggggccaggg tgggggtggg ggtgggggtg 850  
gtggtggggg tagtggcctt tgctgtgtgc caccctccct gtaagtctat 900  
ttaaaaacat cgacgataca ttgaaatgtg tgaacgtttt gaaaagctac 950  
agcttccagc agccaaaagc aactgttggt ttggcaagac ggtcctgatg 1000  
tacaagcttg attgaaattc actgctcact tgatacgtta ttcagaaacc 1050  
caaggaatgg ctgtcccat cctcatgtgg ctgtgtggag ctcagctgtg 1100  
ttgtgtggca gtttattaaa ctgtcccca gatcgacacg caaaaaaaaa 1150

<210> 372

<211> 269

<212> PRT

<213> Homo sapiens

<400> 372

Met	Ala	Ala	Ala	Ser	Ala	Gly	Ala	Thr	Arg	Leu	Leu	Leu	Leu	Leu
1				5					10					15
Leu	Met	Ala	Val	Ala	Ala	Pro	Ser	Arg	Ala	Arg	Gly	Ser	Gly	Cys
				20					25					30
Arg	Ala	Gly	Thr	Gly	Ala	Arg	Gly	Ala	Gly	Ala	Glu	Gly	Arg	Glu
				35					40					45

Gly	Glu	Ala	Cys	Gly	Thr	Val	Gly	Leu	Leu	Leu	Glu	His	Ser	Phe	
				50					55					60	
Glu	Ile	Asp	Asp	Ser	Ala	Asn	Phe	Arg	Lys	Arg	Gly	Ser	Leu	Leu	
				65					70					75	
Trp	Asn	Gln	Gln	Asp	Gly	Thr	Leu	Ser	Leu	Ser	Gln	Arg	Gln	Leu	
				80					85					90	
Ser	Glu	Glu	Glu	Arg	Gly	Arg	Leu	Arg	Asp	Val	Ala	Ala	Leu	Asn	
				95					100					105	
Gly	Leu	Tyr	Arg	Val	Arg	Ile	Pro	Arg	Arg	Pro	Gly	Ala	Leu	Asp	
				110					115					120	
Gly	Leu	Glu	Ala	Gly	Gly	Tyr	Val	Ser	Ser	Phe	Val	Pro	Ala	Cys	
				125					130					135	
Ser	Leu	Val	Glu	Ser	His	Leu	Ser	Asp	Gln	Leu	Thr	Leu	His	Val	
				140					145					150	
Asp	Val	Ala	Gly	Asn	Val	Val	Gly	Val	Ser	Val	Val	Thr	His	Pro	
				155					160					165	
Gly	Gly	Cys	Arg	Gly	His	Glu	Val	Glu	Asp	Val	Asp	Leu	Glu	Leu	
				170					175					180	
Phe	Asn	Thr	Ser	Val	Gln	Leu	Gln	Pro	Pro	Thr	Thr	Ala	Pro	Gly	
				185					190					195	
Pro	Glu	Thr	Ala	Ala	Phe	Ile	Glu	Arg	Leu	Glu	Met	Glu	Gln	Ala	
				200					205					210	
Gln	Lys	Ala	Lys	Asn	Pro	Gln	Glu	Gln	Lys	Ser	Phe	Phe	Ala	Lys	
				215					220					225	
Tyr	Trp	Met	Tyr	Ile	Ile	Pro	Val	Val	Leu	Phe	Leu	Met	Met	Ser	
				230					235					240	
Gly	Ala	Pro	Asp	Thr	Gly	Gly	Gln	Gly	Gly	Gly	Gly	Gly	Gly	Gly	
				245					250					255	
Gly	Gly	Gly	Gly	Ser	Gly	Leu	Cys	Cys	Val	Pro	Pro	Ser	Leu		
				260					265						

<210> 373  
 <211> 1706  
 <212> DNA  
 <213> Homo sapiens

<400> 373  
 ggagcgctgc tggaaccgga gccggagccg gagccacagc ggggaggggtg 50  
 gcctggcggc ctggagccgg acgtgtccgg ggcgtccccg cagaccgggg 100  
 cagcaggtcg tccggggggc caccatgctg gtgactgcct accttgcttt 150  
 tgtaggcctc ctggcctcct gcctggggct ggaactgtca agatgccggg 200





ctctgtgtta ctccattta gaaaataaac acttttaaataat gatcaaaaaa 1700

aaaaaa 1706

<210> 374

<211> 450

<212> PRT

<213> Homo sapiens

<400> 374

Met	Leu	Val	Thr	Ala	Tyr	Leu	Ala	Phe	Val	Gly	Leu	Leu	Ala	Ser
1				5					10					15

Cys	Leu	Gly	Leu	Glu	Leu	Ser	Arg	Cys	Arg	Ala	Lys	Pro	Pro	Gly
				20					25					30

Arg	Ala	Cys	Ser	Asn	Pro	Ser	Phe	Leu	Arg	Phe	Gln	Leu	Asp	Phe
				35					40					45

Tyr	Gln	Val	Tyr	Phe	Leu	Ala	Leu	Ala	Ala	Asp	Trp	Leu	Gln	Ala
				50					55					60

Pro	Tyr	Leu	Tyr	Lys	Leu	Tyr	Gln	His	Tyr	Tyr	Phe	Leu	Glu	Gly
				65					70					75

Gln	Ile	Ala	Ile	Leu	Tyr	Val	Cys	Gly	Leu	Ala	Ser	Thr	Val	Leu
				80					85					90

Phe	Gly	Leu	Val	Ala	Ser	Ser	Leu	Val	Asp	Trp	Leu	Gly	Arg	Lys
				95					100					105

Asn	Ser	Cys	Val	Leu	Phe	Ser	Leu	Thr	Tyr	Ser	Leu	Cys	Cys	Leu
				110					115					120

Thr	Lys	Leu	Ser	Gln	Asp	Tyr	Phe	Val	Leu	Leu	Val	Gly	Arg	Ala
				125					130					135

Leu	Gly	Gly	Leu	Ser	Thr	Ala	Leu	Leu	Phe	Ser	Ala	Phe	Glu	Ala
				140					145					150

Trp	Tyr	Ile	His	Glu	His	Val	Glu	Arg	His	Asp	Phe	Pro	Ala	Glu
				155					160					165

Trp	Ile	Pro	Ala	Thr	Phe	Ala	Arg	Ala	Ala	Phe	Trp	Asn	His	Val
				170					175					180

Leu	Ala	Val	Val	Ala	Gly	Val	Ala	Ala	Glu	Ala	Val	Ala	Ser	Trp
				185					190					195

Ile	Gly	Leu	Gly	Pro	Val	Ala	Pro	Phe	Val	Ala	Ala	Ile	Pro	Leu
				200					205					210

Leu	Ala	Leu	Ala	Gly	Ala	Leu	Ala	Leu	Arg	Asn	Trp	Gly	Glu	Asn
				215					220					225

Tyr	Asp	Arg	Gln	Arg	Ala	Phe	Ser	Arg	Thr	Cys	Ala	Gly	Gly	Leu
				230					235					240

Arg Cys Leu Leu Ser Asp Arg Arg Val	Leu Leu Leu Gly Thr	Ile
245	250	255
Gln Ala Leu Phe Glu Ser Val Ile Phe	Ile Phe Val Phe Leu Trp	
260	265	270
Thr Pro Val Leu Asp Pro His Gly Ala	Pro Leu Gly Ile Ile Phe	
275	280	285
Ser Ser Phe Met Ala Ala Ser Leu Leu	Gly Ser Ser Leu Tyr Arg	
290	295	300
Ile Ala Thr Ser Lys Arg Tyr His Leu	Gln Pro Met His Leu Leu	
305	310	315
Ser Leu Ala Val Leu Ile Val Val Phe	Ser Leu Phe Met Leu Thr	
320	325	330
Phe Ser Thr Ser Pro Gly Gln Glu Ser	Pro Val Glu Ser Phe Ile	
335	340	345
Ala Phe Leu Leu Ile Glu Leu Ala Cys	Gly Leu Tyr Phe Pro Ser	
350	355	360
Met Ser Phe Leu Arg Arg Lys Val Ile	Pro Glu Thr Glu Gln Ala	
365	370	375
Gly Val Leu Asn Trp Phe Arg Val Pro	Leu His Ser Leu Ala Cys	
380	385	390
Leu Gly Leu Leu Val Leu His Asp Ser	Asp Arg Lys Thr Gly Thr	
395	400	405
Arg Asn Met Phe Ser Ile Cys Ser Ala	Val Met Val Met Ala Leu	
410	415	420
Leu Ala Val Val Gly Leu Phe Thr Val	Val Arg His Asp Ala Glu	
425	430	435
Leu Arg Val Pro Ser Pro Thr Glu Glu	Pro Tyr Ala Pro Glu Leu	
440	445	450

<210> 375  
 <211> 1098  
 <212> DNA  
 <213> Artificial

<400> 375  
 gcgacgcgcg gcggggcggc gagaggaaac gcggcgccgg gccgggcccg 50  
 gccctggaga tgggtccccg cgccgcgggc tgggtgtgtc tcgtgctctg 100  
 gctccccgcg tgcgtcgcgg ccacaggctt ccgtatccat gattatttgt 150  
 actttcaagt gctgagtcct ggggacattc gatacatctt cacagccaca 200  
 cctgccaaagg actttggtgg tatctttcac acaaggtatg agcagattca 250

ccttgtcccc gctgaacctc cagaggcctg cggggaactc agcaacggtt 300  
 tottcatcca ggaccagatt gctctggtgg agaggggggg ctgctccttc 350  
 ctctccaaga ctcggttggt ccaggagcac ggcgggcggg cggtgatcat 400  
 ctctgacaac gcagttgaca atgacagctt ctacgtggag atgatccagg 450  
 acagtaccca gcgcacagct gacatccccg ccctcttcct gctcggccga 500  
 gacggctaca tgatccgcgg ctctctggaa cagcatgggc tgccatgggc 550  
 catcatttcc atccagtcga atgtcaccag catccccacc tttgagctgc 600  
 tgcaaccgcc ctggaccttc tggtagaaga gtttgtccca cattccagcc 650  
 ataagtgact ctgagctggg aaggggaaac ccaggaattt tgctacttgg 700  
 aatttgagaga tagcatctgg ggacaagtgg agccaggtag aggaaaaggg 750  
 tttgggcgtt gctaggctga aagggaagcc acaccactgg ccttcccttc 800  
 cccaggggccc ccaagggtgt ctcatgctac aagaagaggc aagagacagg 850  
 cccaggggct tctggctaga acccgaaaca aaaggagctg aaggcaggtg 900  
 gcctgagagc catctgtgac ctgtcacact cacctggctc cagcctcccc 950  
 taccagggtt ctctgcacag tgaccttcac agcagttggt ggagtgggtt 1000  
 aaagagctgg tgtttgggga ctcaataaac cctcactgac tttttagcaa 1050  
 taaagcttct catcagggtt gcaaaaaaaaa aaaaaaaaaa aaaaaaaaa 1098

<210> 376  
 <211> 188  
 <212> PRT  
 <213> Homo sapiens

<400> 376  
 Met Val Pro Gly Ala Ala Gly Trp Cys Cys Leu Val Leu Trp Leu  
 1 5 10 15  
 Pro Ala Cys Val Ala Ala His Gly Phe Arg Ile His Asp Tyr Leu  
 20 25 30  
 Tyr Phe Gln Val Leu Ser Pro Gly Asp Ile Arg Tyr Ile Phe Thr  
 35 40 45  
 Ala Thr Pro Ala Lys Asp Phe Gly Gly Ile Phe His Thr Arg Tyr  
 50 55 60  
 Glu Gln Ile His Leu Val Pro Ala Glu Pro Pro Glu Ala Cys Gly  
 65 70 75  
 Glu Leu Ser Asn Gly Phe Phe Ile Gln Asp Gln Ile Ala Leu Val  
 80 85 90

Glu Arg Gly Gly Cys Ser Phe Leu Ser Lys Thr Arg Val Val Gln  
 95 100 105

Glu His Gly Gly Arg Ala Val Ile Ile Ser Asp Asn Ala Val Asp  
 110 115 120

Asn Asp Ser Phe Tyr Val Glu Met Ile Gln Asp Ser Thr Gln Arg  
 125 130 135

Thr Ala Asp Ile Pro Ala Leu Phe Leu Leu Gly Arg Asp Gly Tyr  
 140 145 150

Met Ile Arg Arg Ser Leu Glu Gln His Gly Leu Pro Trp Ala Ile  
 155 160 165

Ile Ser Ile Pro Val Asn Val Thr Ser Ile Pro Thr Phe Glu Leu  
 170 175 180

Leu Gln Pro Pro Trp Thr Phe Trp  
 185

<210> 377  
 <211> 496  
 <212> DNA  
 <213> Artificial

<220>  
 <221> unsure  
 <222> 396  
 <223> unknown base

<400> 377  
 tctgcctcca ctgctctgtg ctgggatcat ggaacttgca ctgctgtgtg 50  
 ggctgggtggt gatggctggt gtgattccaa tccagggcgg gatcctgaac 100  
 ctgaacaaga tgggtcaagca agtgactggg aaaatgccca tcctctccta 150  
 ctggccctac ggctgtcact gcggactagg tggcagaggc caacccaaag 200  
 atgccacgga ctggtgctgc cagacccatg actgctgcta tgaccacctg 250  
 aagacccagg ggtgcggcat ctacaaggac aacaacaaaa gcagcatata 300  
 ttgtatggat ttatctcaac gctattgttt aatggctgtg tttaatgtga 350  
 tctatctgga aaatgaggac tccgaataaa aagctattac tawttnaaaa 400  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 450  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaa 496

<210> 378  
 <211> 116  
 <212> PRT  
 <213> Homo sapiens

<400> 378

Met	Glu	Leu	Ala	Leu	Leu	Cys	Gly	Leu	Val	Val	Met	Ala	Gly	Val
1				5					10					15
Ile	Pro	Ile	Gln	Gly	Gly	Ile	Leu	Asn	Leu	Asn	Lys	Met	Val	Lys
			20						25					30
Gln	Val	Thr	Gly	Lys	Met	Pro	Ile	Leu	Ser	Tyr	Trp	Pro	Tyr	Gly
			35						40					45
Cys	His	Cys	Gly	Leu	Gly	Gly	Arg	Gly	Gln	Pro	Lys	Asp	Ala	Thr
			50						55					60
Asp	Trp	Cys	Cys	Gln	Thr	His	Asp	Cys	Cys	Tyr	Asp	His	Leu	Lys
			65						70					75
Thr	Gln	Gly	Cys	Gly	Ile	Tyr	Lys	Asp	Asn	Asn	Lys	Ser	Ser	Ile
			80						85					90
His	Cys	Met	Asp	Leu	Ser	Gln	Arg	Tyr	Cys	Leu	Met	Ala	Val	Phe
			95						100					105
Asn	Val	Ile	Tyr	Leu	Glu	Asn	Glu	Asp	Ser	Glu				
			110						115					

<210> 379  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 379  
 ctgcctccac tgctctgtgc tggg 24

<210> 380  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 380  
 cagagcagtg gatgttcccc tggg 24

<210> 381  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45

<223> Synthetic construct.

<400> 381

ctgaacaaga tggtaagca agtgactggg aaaatgccca tcctc 45

<210> 382

<211> 764

<212> DNA

<213> Homo sapiens

<400> 382

ctcgcttctt ccttctggat gggggcccag gggggcccagg agagtataaa 50  
ggcgtatgtg aggtgccccg gcacaaccag acgcccagtc acaggcgaga 100  
gccctgggat gcaccggcca gaggccatgc tgctgctgct cacgcttgcc 150  
ctcctggggg gccccacctg ggcagggaag atgtatggcc ctggaggagg 200  
caagtatttc agcaccactg aagactacga ccatgaaatc acagggctgc 250  
gggtgtctgt aggtcttctc ctggtgaaaa gtgtccaggt gaaacttgga 300  
gactcctggg acgtgaaact gggagcctta ggtgggaata cccaggaagt 350  
caccctgcag ccaggcgaat acatcacaaa agtctttgtc gccttccaag 400  
ctttcctccg gggatgggc atgtacacca gcaaggaccg ctatttctat 450  
tttggaagc ttgatggcca gatctcctct gcctaccca gccaaaggagg 500  
gcaggtgctg gtgggcatct atggccagta tcaactcctt ggcataaga 550  
gcattggctt tgaatggaat tatccactag aggagccgac cactgagcca 600  
ccagttaatc tcacatactc agcaaactca cccgtgggtc gctaggggtg 650  
ggtatggggc catccgagct gaggccatct gtgtgggtgt ggctgatggt 700  
actggagtaa ctgagtcggg acgctgaatc tgaatccacc aataaataaa 750  
gcttctgcag aaaa 764

<210> 383

<211> 178

<212> PRT

<213> Homo sapiens

<400> 383

Met	His	Arg	Pro	Glu	Ala	Met	Leu	Leu	Leu	Leu	Thr	Leu	Ala	Leu
1				5					10					15
Leu	Gly	Gly	Pro	Thr	Trp	Ala	Gly	Lys	Met	Tyr	Gly	Pro	Gly	Gly
			20						25					30
Gly	Lys	Tyr	Phe	Ser	Thr	Thr	Glu	Asp	Tyr	Asp	His	Glu	Ile	Thr
			35						40					45

Gly Leu Arg Val Ser Val Gly Leu Leu Leu Val Lys Ser Val Gln  
50 55 60  
Val Lys Leu Gly Asp Ser Trp Asp Val Lys Leu Gly Ala Leu Gly  
65 70 75  
Gly Asn Thr Gln Glu Val Thr Leu Gln Pro Gly Glu Tyr Ile Thr  
80 85 90  
Lys Val Phe Val Ala Phe Gln Ala Phe Leu Arg Gly Met Val Met  
95 100 105  
Tyr Thr Ser Lys Asp Arg Tyr Phe Tyr Phe Gly Lys Leu Asp Gly  
110 115 120  
Gln Ile Ser Ser Ala Tyr Pro Ser Gln Glu Gly Gln Val Leu Val  
125 130 135  
Gly Ile Tyr Gly Gln Tyr Gln Leu Leu Gly Ile Lys Ser Ile Gly  
140 145 150  
Phe Glu Trp Asn Tyr Pro Leu Glu Glu Pro Thr Thr Glu Pro Pro  
155 160 165  
Val Asn Leu Thr Tyr Ser Ala Asn Ser Pro Val Gly Arg  
170 175

<210> 384  
<211> 2379  
<212> DNA  
<213> Homo sapiens

<400> 384  
gctgagcgtg tgcgcggtac ggggctctcc tgccttctgg gctccaacgc 50  
agctctgtgg ctgaactggg tgctcatcac gggaactgct gggctatgga 100  
atacagatgt ggcagctcag gtagcccaa attgcctgga agaatacatc 150  
atgtttttcg ataagaagaa attgtaggat ccagtttttt ttttaaccgc 200  
ccctcccca cccccaaaa aaactgtaaa gatgcaaaaa cgtaatatcc 250  
atgaagatcc tattacctag gaagattttg atgttttgct gcgaatgcgg 300  
tgttgggatt tatttgttct tggagtgttc tgcgtggctg gcaaagaata 350  
atgttcacaa atcgggtccat ctcccaaggg gtccaatttt tcttctctggg 400  
tgtcagcgcg ccctgactca ctacagtga gctgacagg gctgtcatgc 450  
aactggcccc taagccaaag caaaagacct aaggacgacc tttgaacaat 500  
acaaaggatg ggtttcaatg taattaggct actgagcggg tcagctgtag 550  
cactgggtat agccccact gtcttactga caatgctttc ttctgccgaa 600  
cgaggatgcc ctaagggtg taggtgtgaa ggcaaatgg tatattgtga 650



atctcagaaa ttacaggaga taccctcaag tataatctgct ggttgcttag 700  
 gtttgtccct tcgtataaac agccttcaaa aacttaagta taatcaattt 750  
 aaagggtca accagctcac ctggctatac cttgaccata accatatcag 800  
 caatattgac gaaaatgctt ttaatggaat acgcagactc aaagagctga 850  
 ttcttagttc caatagaatc tcctattttc ttaacaatac cttcagacct 900  
 gtgacaaatt tacggaactt ggatctgtcc tataatcagc tgcatctctt 950  
 gggatctgaa cagtttcggg gcttgcgaa gctgctgagt ttacatttac 1000  
 ggtctaactc cctgagaacc atccctgtgc gaatattcca agactgccgc 1050  
 aacctggaac ttttggaact gggatataac cggatccgaa gtttagccag 1100  
 gaatgtcttt gctggcatga tcagactcaa agaacttcac ctggagcaca 1150  
 atcaattttc caagctcaac ctggcccttt ttccaagggt ggtcagcctt 1200  
 cagaaccttt acttgacgtg gaataaaatc agtgtcatag gacagaccat 1250  
 gtccctggacc tggagctcct taaaaaggct tgatttatca ggcaatgaga 1300  
 tcgaagcttt cagtggacct agtggtttcc agtgtgtccc gaatctgcag 1350  
 cgcctcaacc tggattccaa caagctcaca ttatttggtc aagagatttt 1400  
 ggattcttgg atatccctca atgacatcag tcttgctggg aatatatggg 1450  
 aatgcagcag aaatatttgc tcccttgtaa actggctgaa aagttttaaa 1500  
 ggtctaaggg agaatacaat tatctgtgcc agtcccaaag agctgcaagg 1550  
 agtaaagtgt atcgatgcag tgaagaacta cagcatctgt ggcaaaagta 1600  
 ctacagagag gtttgatctg gccagggctc tcccaaagcc gacgtttaag 1650  
 cccaagctcc ccaggccgaa gcatgagagc aaacccccct tgcccccgac 1700  
 ggtgggagcc acagagcccg gccagagac cgatgctgac gccgagcaca 1750  
 tctctttcca taaaatcatc gcgggcagcg tggcgctttt cctgtccgtg 1800  
 ctcgatcatc tgctgggtat ctacgtgtca tggaagcggg accctgagag 1850  
 catgaagcag ctgcagcagc gctccctcat gcgaaggcac aggaaaaaga 1900  
 aaagacagtc octaaagcaa atgactccca gcaccagga attttatgta 1950  
 gattataaac ccaccaacac ggagaccagc gagatgctgc tgaatgggac 2000  
 gggaccctgc acctataaca aatcgggctc caggagagtgt gaggtatgaa 2050  
 ccattgtgat aaaaagagct cttaaagct gggaaataag tgggtgcttta 2100



		200							205						210
His	Leu	Glu	His	Asn	Gln	Phe	Ser	Lys	Leu	Asn	Leu	Ala	Leu	Phe	
		215							220					225	
Pro	Arg	Leu	Val	Ser	Leu	Gln	Asn	Leu	Tyr	Leu	Gln	Trp	Asn	Lys	
		230							235					240	
Ile	Ser	Val	Ile	Gly	Gln	Thr	Met	Ser	Trp	Thr	Trp	Ser	Ser	Leu	
		245							250					255	
Gln	Arg	Leu	Asp	Leu	Ser	Gly	Asn	Glu	Ile	Glu	Ala	Phe	Ser	Gly	
		260							265					270	
Pro	Ser	Val	Phe	Gln	Cys	Val	Pro	Asn	Leu	Gln	Arg	Leu	Asn	Leu	
		275							280					285	
Asp	Ser	Asn	Lys	Leu	Thr	Phe	Ile	Gly	Gln	Glu	Ile	Leu	Asp	Ser	
		290							295					300	
Trp	Ile	Ser	Leu	Asn	Asp	Ile	Ser	Leu	Ala	Gly	Asn	Ile	Trp	Glu	
		305							310					315	
Cys	Ser	Arg	Asn	Ile	Cys	Ser	Leu	Val	Asn	Trp	Leu	Lys	Ser	Phe	
		320							325					330	
Lys	Gly	Leu	Arg	Glu	Asn	Thr	Ile	Ile	Cys	Ala	Ser	Pro	Lys	Glu	
		335							340					345	
Leu	Gln	Gly	Val	Asn	Val	Ile	Asp	Ala	Val	Lys	Asn	Tyr	Ser	Ile	
		350							355					360	
Cys	Gly	Lys	Ser	Thr	Thr	Glu	Arg	Phe	Asp	Leu	Ala	Arg	Ala	Leu	
		365							370					375	
Pro	Lys	Pro	Thr	Phe	Lys	Pro	Lys	Leu	Pro	Arg	Pro	Lys	His	Glu	
		380							385					390	
Ser	Lys	Pro	Pro	Leu	Pro	Pro	Thr	Val	Gly	Ala	Thr	Glu	Pro	Gly	
		395							400					405	
Pro	Glu	Thr	Asp	Ala	Asp	Ala	Glu	His	Ile	Ser	Phe	His	Lys	Ile	
		410							415					420	
Ile	Ala	Gly	Ser	Val	Ala	Leu	Phe	Leu	Ser	Val	Leu	Val	Ile	Leu	
		425							430					435	
Leu	Val	Ile	Tyr	Val	Ser	Trp	Lys	Arg	Tyr	Pro	Ala	Ser	Met	Lys	
		440							445					450	
Gln	Leu	Gln	Gln	Arg	Ser	Leu	Met	Arg	Arg	His	Arg	Lys	Lys	Lys	
		455							460					465	
Arg	Gln	Ser	Leu	Lys	Gln	Met	Thr	Pro	Ser	Thr	Gln	Glu	Phe	Tyr	
		470							475					480	
Val	Asp	Tyr	Lys	Pro	Thr	Asn	Thr	Glu	Thr	Ser	Glu	Met	Leu	Leu	
		485							490					495	

Asn Gly Thr Gly Pro Cys Thr Tyr Asn Lys Ser Gly Ser Arg Glu  
 500 505 510

Cys Glu Val

<210> 386  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 386  
 ctgggatctg aacagtttcg gggc 24

<210> 387  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 387  
 ggtccccagg acatggtctg tccc 24

<210> 388  
 <211> 48  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-48  
 <223> Synthetic construct.

<400> 388  
 gctgagttta catttacggt ctaactccct gagaaccatc cctgtgcg 48

<210> 389  
 <211> 1449  
 <212> DNA  
 <213> Homo sapiens

<400> 389  
 agttctgaga aagaaggaaa taaacacagg caccaaacca ctatcctaag 50  
 ttgactgtcc tttaaatatg tcaagatcca gacttttcag tgtcacctca 100  
 gcgatctcaa cgatagggat cttgtgtttg ccgctattcc agttggtgct 150  
 ctcggaccta ccatgcgaag aagatgaaat gtgtgtaaat tataatgacc 200



Ile	Gly	Ile	Leu	Cys	Leu	Pro	Leu	Phe	Gln	Leu	Val	Leu	Ser	Asp	
				20					25					30	
Leu	Pro	Cys	Glu	Glu	Asp	Glu	Met	Cys	Val	Asn	Tyr	Asn	Asp	Gln	
			35						40					45	
His	Pro	Asn	Gly	Trp	Tyr	Ile	Trp	Ile	Leu	Leu	Leu	Leu	Val	Leu	
			50						55					60	
Val	Ala	Ala	Leu	Leu	Cys	Gly	Ala	Val	Val	Leu	Cys	Leu	Gln	Cys	
			65						70					75	
Trp	Leu	Arg	Arg	Pro	Arg	Ile	Asp	Ser	His	Arg	Arg	Thr	Met	Ala	
				80					85					90	
Val	Phe	Ala	Val	Gly	Asp	Leu	Asp	Ser	Ile	Tyr	Gly	Thr	Glu	Ala	
				95					100					105	
Ala	Val	Ser	Pro	Thr	Val	Gly	Ile	His	Leu	Gln	Thr	Gln	Thr	Pro	
				110					115					120	
Asp	Leu	Tyr	Pro	Val	Pro	Ala	Pro	Cys	Phe	Gly	Pro	Leu	Gly	Ser	
				125					130					135	
Pro	Pro	Pro	Tyr	Glu	Glu	Ile	Val	Lys	Thr	Thr					
				140					145						

<210> 391  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
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 <222> 1-26  
 <223> Synthetic construct.

<400> 391  
 cttttcagtg tcacctcagc gatctc 26

<210> 392  
 <211> 23  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-23  
 <223> Synthetic construct.

<400> 392  
 ccaaaacatg gagcaggaac agg 23

<210> 393  
 <211> 47  
 <212> DNA  
 <213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-47  
<223> Synthetic construct.

<400> 393  
ccagttggtg ctctcggacc taccatgcga agaagatgaa atgtgtg 47

<210> 394  
<211> 2340  
<212> DNA  
<213> Homo sapiens

<400> 394  
gagcggagta aaatctccac aagctgggaa caaacctcgt cccaactccc 50  
accacccggc gtttctccag ctcgatctgg aggctgcttc gccagtgtgg 100  
gacgcagctg acgcccgtt attagctctc gctgcgtcgc cccggctcag 150  
aagctccgtg gcggcggcga ccgtgacgag aagcccacgg ccagctcagt 200  
tctcttctac tttgggagag agagaaagtc agatgccctt tttaaactcc 250  
ctcttcaaaa ctcatctcct gggtgactga gttaatagag tggatacaac 300  
cttgctgaag atgaagaata tacaatattg aggatatttt tttctttttt 350  
ttttcaagtc ttgatttgtg gcttaoctca agttaccatt tttcagtcaa 400  
gtctgtttgt ttgcttcttc agaaatgttt tttacaatct caagaaaaaa 450  
tatgtcccag aaattgagtt tactgttgct tgtatttgga ctatttggg 500  
gattgatgtt actgcactat acttttcaac aaccaagaca tcaaagcagt 550  
gtcaagttac gtgagcaaact actagactta agcaaaagat atgttaaagc 600  
tctagcagag gaaaataaga acacagtggg tgtcgagaac ggtgcttcta 650  
tggcaggata tgcggatctg aaaagaacaa ttgctgtcct tctggatgac 700  
attttgcaac gattggtgaa gctggagAAC aaagttgact atattgttgt 750  
gaatggctca gcagccaaca ccaccaatgg tactagtggg aatttgggtc 800  
cagtaaccac aaataaaaaga acgaatgtct cgggcagtat cagatagcag 850  
ttgaaaatca ccttggtgtg ctccatccac tgtggattat atcctatggc 900  
agaaaagctt tataattgct ggcttaggac agagcaatac tttacaataa 950  
aagctctaca catTTTcaag gagtatgctg gattcatgga actctaattc 1000  
tgtacataaa aattttaaag ttatttgttt gctttcaggc aagtctgttc 1050  
aatgctgtac tatgtcctta aagagaattt ggtaacttgg ttgatgtggt 1100





Leu Leu Leu Leu Val Phe Gly Leu Ile Trp Gly Leu Met Leu Leu  
20 25 30  
His Tyr Thr Phe Gln Gln Pro Arg His Gln Ser Ser Val Lys Leu  
35 40 45  
Arg Glu Gln Ile Leu Asp Leu Ser Lys Arg Tyr Val Lys Ala Leu  
50 55 60  
Ala Glu Glu Asn Lys Asn Thr Val Asp Val Glu Asn Gly Ala Ser  
65 70 75  
Met Ala Gly Tyr Ala Asp Leu Lys Arg Thr Ile Ala Val Leu Leu  
80 85 90  
Asp Asp Ile Leu Gln Arg Leu Val Lys Leu Glu Asn Lys Val Asp  
95 100 105  
Tyr Ile Val Val Asn Gly Ser Ala Ala Asn Thr Thr Asn Gly Thr  
110 115 120  
Ser Gly Asn Leu Val Pro Val Thr Thr Asn Lys Arg Thr Asn Val  
125 130 135  
Ser Gly Ser Ile Arg  
140

<210> 396  
<211> 2639  
<212> DNA  
<213> Homo sapiens

<400> 396  
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gggcccagac aaccgggcca tgcttccccg ggtgccaatg cgaggtggag 150  
accttcggcc ttttcgacag cttcagcctg actcgggtgg attgtagcgg 200  
cctgggcccc cacatcatgc cggtgcccat ccctctggac acagcccact 250  
tggacctgtc ctccaaccgg ctggagatgg tgaatgagtc ggtgttggcg 300  
gggcccgggct acacgacgtt ggctggcctg gatctcagcc acaacctgct 350  
caccagcatc taccctaactg ctttctccc ctttcgctac ctggagtcgc 400  
ttgacctcag ccacaatggc ctgacagccc tgccagccga gagcttcacc 450  
agctcacccc tgagcgacgt gaaccttagc cacaaccagc tccgggaggt 500  
ctcagtgtct gccttcacga cgcacagtca gggccgggca ctacacgtgg 550  
acctctccca caacctcatt caccgcctcg tgccccaccc cagaggggcc 600  
ggcctgcctg cgcccacat tcagagcctg aacctggcct ggaaccggct 650





Phe Thr Thr His Ser Gln Gly Arg Ala Leu His Val Asp Leu Ser  
155 160 165

His Asn Leu Ile His Arg Leu Val Pro His Pro Thr Arg Ala Gly  
170 175 180

Leu Pro Ala Pro Thr Ile Gln Ser Leu Asn Leu Ala Trp Asn Arg  
185 190 195

Leu His Ala Val Pro Asn Leu Arg Asp Leu Pro Leu Arg Tyr Leu  
200 205 210

Ser Leu Asp Gly Asn Pro Leu Ala Val Ile Gly Pro Gly Ala Phe  
215 220 225

Ala Gly Leu Gly Gly Leu Thr His Leu Ser Leu Ala Ser Leu Gln  
230 235 240

Arg Leu Pro Glu Leu Ala Pro Ser Gly Phe Arg Glu Leu Pro Gly  
245 250 255

Leu Gln Val Leu Asp Leu Ser Gly Asn Pro Lys Leu Asn Trp Ala  
260 265 270

Gly Ala Glu Val Phe Ser Gly Leu Ser Ser Leu Gln Glu Leu Asp  
275 280 285

Leu Ser Gly Thr Asn Leu Val Pro Leu Pro Glu Ala Leu Leu Leu  
290 295 300

His Leu Pro Ala Leu Gln Ser Val Ser Val Gly Gln Asp Val Arg  
305 310 315

Cys Arg Arg Leu Val Arg Glu Gly Thr Tyr Pro Arg Arg Pro Gly  
320 325 330

Ser Ser Pro Lys Val Pro Leu His Cys Val Asp Thr Arg Glu Ser  
335 340 345

Ala Ala Arg Gly Pro Thr Ile Leu  
350

<210> 398  
<211> 23  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-23  
<223> Synthetic construct.

<400> 398  
ccctgccagc cgagagcttc acc 23

<210> 399  
<211> 23  
<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-23

<223> Synthetic construct.

<400> 399

ggttggtgcc cgaaaggtcc agc 23

<210> 400

<211> 44

<212> DNA

<213> Artificial

<220>

<221> Artificial Sequence

<222> 1-44

<223> Synthetic construct.

<400> 400

caacccaag cttaactggg caggagctga ggtgttttca ggcc 44

<210> 401

<211> 1571

<212> DNA

<213> Homo sapiens

<400> 401

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 atgtcattct ctatctattc actgcaagtg cctgctgttc caggccttac 200  
 ctgctgggca ctaacggcgg agccaggatg gggacagaat aaaggagcca 250  
 cgacctgtgc caccaactcg cactcagact ctgaactcag acctgaaatc 300  
 ttctcttcac gggaggcttg gcagtttttc ttactcctgt ggtctccaga 350  
 tttcaggcct aagatgaaag cctctagtct tgccttcagc cttctctctg 400  
 ctgcgtttta tctcctatgg actccttcca ctggactgaa gacactcaat 450  
 ttgggaagct gtgtgatgc cacaacctt caggaaatac gaaatggatt 500  
 ttctgagata cggggcagtg tgcaagccaa agatggaaac attgacatca 550  
 gaatcttaag gaggactgag tctttgcaag acacaaagcc tgcaatcga 600  
 tgctgcctcc tgcgccattt gctaagactc tatctggaca gggattttaa 650  
 aaactaccag acccctgacc attatactct ccggaagatc agcagcctcg 700  
 ccaattcctt tcttaccatc aagaaggacc tccggctctc tcatgccac 750

atgacatgcc attgtgggga ggaagcaatg aagaaataca gccagattct 800  
gagtcacttt gaaaagctgg aacctcaggc agcagttgtg aaggctttgg 850  
gggaactaga cattcttctg caatggatgg aggagacaga ataggaggaa 900  
agtgatgctg ctgctaagaa tattcgaggt caagagctcc agtcttcaat 950  
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atTTTTgtaa tatctttctg ctattggata tttttattag ttaatatatt 1150  
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ctttaaaaaa attcacagat tatatttata acctgactag agcaggtgat 1250  
gtatttttat acagtaaaaa aaaaaaacct tgtaaattct agaagagtgg 1300  
ctaggggggggt tattcatttg tattcaacta aggacatatt tactcatgct 1350  
gatgctctgt gagatatttg aaattgaacc aatgactact taggatgggt 1400  
tgtggaataa gttttgatgt ggaattgcac atctacctta caattactga 1450  
ccatccccag tagactcccc agtcccataa ttgtgtatct tccagccagg 1500  
aatcctacac ggccagcatg tatttctaca aataaagttt tctttgcata 1550  
ccaaaaaaaa aaaaaaaaaa a 1571

<210> 402  
<211> 261  
<212> PRT  
<213> Homo sapiens

<400> 402  
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Ser Phe Ser Ile Tyr Ser Leu Gln Val Pro Ala Val Pro Gly Leu  
20 25 30  
Thr Cys Trp Ala Leu Thr Ala Glu Pro Gly Trp Gly Gln Asn Lys  
35 40 45  
Gly Ala Thr Thr Cys Ala Thr Asn Ser His Ser Asp Ser Glu Leu  
50 55 60  
Arg Pro Glu Ile Phe Ser Ser Arg Glu Ala Trp Gln Phe Phe Leu  
65 70 75  
Leu Leu Trp Ser Pro Asp Phe Arg Pro Lys Met Lys Ala Ser Ser  
80 85 90

Leu	Ala	Phe	Ser	Leu	Leu	Ser	Ala	Ala	Phe	Tyr	Leu	Leu	Trp	Thr
				95					100					105
Pro	Ser	Thr	Gly	Leu	Lys	Thr	Leu	Asn	Leu	Gly	Ser	Cys	Val	Ile
				110					115					120
Ala	Thr	Asn	Leu	Gln	Glu	Ile	Arg	Asn	Gly	Phe	Ser	Glu	Ile	Arg
				125					130					135
Gly	Ser	Val	Gln	Ala	Lys	Asp	Gly	Asn	Ile	Asp	Ile	Arg	Ile	Leu
				140					145					150
Arg	Arg	Thr	Glu	Ser	Leu	Gln	Asp	Thr	Lys	Pro	Ala	Asn	Arg	Cys
				155					160					165
Cys	Leu	Leu	Arg	His	Leu	Leu	Arg	Leu	Tyr	Leu	Asp	Arg	Val	Phe
				170					175					180
Lys	Asn	Tyr	Gln	Thr	Pro	Asp	His	Tyr	Thr	Leu	Arg	Lys	Ile	Ser
				185					190					195
Ser	Leu	Ala	Asn	Ser	Phe	Leu	Thr	Ile	Lys	Lys	Asp	Leu	Arg	Leu
				200					205					210
Ser	His	Ala	His	Met	Thr	Cys	His	Cys	Gly	Glu	Glu	Ala	Met	Lys
				215					220					225
Lys	Tyr	Ser	Gln	Ile	Leu	Ser	His	Phe	Glu	Lys	Leu	Glu	Pro	Gln
				230					235					240
Ala	Ala	Val	Val	Lys	Ala	Leu	Gly	Glu	Leu	Asp	Ile	Leu	Leu	Gln
				245					250					255
Trp	Met	Glu	Glu	Thr	Glu									
				260										

<210> 403  
 <211> 28  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-28  
 <223> Synthetic construct.

<400> 403  
 ctccctgtgggt ctccagattt caggccta 28

<210> 404  
 <211> 26  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-26  
 <223> Synthetic construct.

<400> 404  
agtcctcctt aagattctga tgtcaa 26

<210> 405  
<211> 998  
<212> DNA  
<213> Homo sapiens

<400> 405  
ccgttatcgt cttgcgctac tgctgaatgt ccgtcccga ggaggaggag 50  
aggcttttgc cgctgaccca gagatggccc cgagcgagca aattcctact 100  
gtccggctgc gcggtaccg tggccgagct agcaaccttt cccctggatc 150  
tcacaaaaac tcgactccaa atgcaaggag aagcagctct tgctcggttg 200  
ggagacggtg caagagaatc tgccccctat aggggaatgg tgcgcacagc 250  
cctagggatc attgaagagg aaggctttct aaagctttgg caaggagtga 300  
caccgcccat ttacagacac gtagtgtatt ctggaggctg aatggtcaca 350  
tatgaacatc tccgagaggt tgtgtttggc aaaagtgaag atgagcatta 400  
tcccctttgg aaatcagtca ttggagggat gatggctggt gttattggcc 450  
agtttttagc caatccaact gacctagtga aggttcagat gcaaatggaa 500  
ggaaaaagga aactggaagg aaaaccattg cgatttcgtg gtgtacatca 550  
tgcatttgca aaaatcctag ctgaaggagg aatacgaggg ctttgggcag 600  
gctgggtacc caatatacaa agagcagcac tggatgaatat gggagattta 650  
accacttatg atacagtga acactacttg gtattgaata caccacttga 700  
ggacaatatc atgactcacg gtttatcaag tttatgttct ggactggtag 750  
cttctattct gggaacacca gccgatgtca tcaaaagcag aataatgaat 800  
caaccacgag ataaacaagg aaggggactt ttgtataaat catcgactga 850  
ctgcttgatt caggctgttc aaggtgaagg attcatgagt ctatataaag 900  
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cttacttatg aaaaaatcag agagatgagt ggagtcagtc cattttaa 998

<210> 406  
<211> 323  
<212> PRT  
<213> Homo sapiens

<400> 406  
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1 5 10 15



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				20					25					30	
Thr	Val	Ala	Glu	Leu	Ala	Thr	Phe	Pro	Leu	Asp	Leu	Thr	Lys	Thr	
				35					40					45	
Arg	Leu	Gln	Met	Gln	Gly	Glu	Ala	Ala	Leu	Ala	Arg	Leu	Gly	Asp	
				50					55					60	
Gly	Ala	Arg	Glu	Ser	Ala	Pro	Tyr	Arg	Gly	Met	Val	Arg	Thr	Ala	
				65					70					75	
Leu	Gly	Ile	Ile	Glu	Glu	Glu	Gly	Phe	Leu	Lys	Leu	Trp	Gln	Gly	
				80					85					90	
Val	Thr	Pro	Ala	Ile	Tyr	Arg	His	Val	Val	Tyr	Ser	Gly	Gly	Arg	
				95					100					105	
Met	Val	Thr	Tyr	Glu	His	Leu	Arg	Glu	Val	Val	Phe	Gly	Lys	Ser	
				110					115					120	
Glu	Asp	Glu	His	Tyr	Pro	Leu	Trp	Lys	Ser	Val	Ile	Gly	Gly	Met	
				125					130					135	
Met	Ala	Gly	Val	Ile	Gly	Gln	Phe	Leu	Ala	Asn	Pro	Thr	Asp	Leu	
				140					145					150	
Val	Lys	Val	Gln	Met	Gln	Met	Glu	Gly	Lys	Arg	Lys	Leu	Glu	Gly	
				155					160					165	
Lys	Pro	Leu	Arg	Phe	Arg	Gly	Val	His	His	Ala	Phe	Ala	Lys	Ile	
				170					175					180	
Leu	Ala	Glu	Gly	Gly	Ile	Arg	Gly	Leu	Trp	Ala	Gly	Trp	Val	Pro	
				185					190					195	
Asn	Ile	Gln	Arg	Ala	Ala	Leu	Val	Asn	Met	Gly	Asp	Leu	Thr	Thr	
				200					205					210	
Tyr	Asp	Thr	Val	Lys	His	Tyr	Leu	Val	Leu	Asn	Thr	Pro	Leu	Glu	
				215					220					225	
Asp	Asn	Ile	Met	Thr	His	Gly	Leu	Ser	Ser	Leu	Cys	Ser	Gly	Leu	
				230					235					240	
Val	Ala	Ser	Ile	Leu	Gly	Thr	Pro	Ala	Asp	Val	Ile	Lys	Ser	Arg	
				245					250					255	
Ile	Met	Asn	Gln	Pro	Arg	Asp	Lys	Gln	Gly	Arg	Gly	Leu	Leu	Tyr	
				260					265					270	
Lys	Ser	Ser	Thr	Asp	Cys	Leu	Ile	Gln	Ala	Val	Gln	Gly	Glu	Gly	
				275					280					285	
Phe	Met	Ser	Leu	Tyr	Lys	Gly	Phe	Leu	Pro	Ser	Trp	Leu	Arg	Met	
				290					295					300	
Thr	Pro	Trp	Ser	Met	Val	Phe	Trp	Leu	Thr	Tyr	Glu	Lys	Ile	Arg	

305

310

315

Glu Met Ser Gly Val Ser Pro Phe  
320

<210> 407  
<211> 31  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-31  
<223> Synthetic construct.

<400> 407  
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<210> 408  
<211> 34  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-34  
<223> Synthetic construct.

<400> 408  
gcggaattct taaaatggac tgactocact catc 34

<210> 409  
<211> 1487  
<212> DNA  
<213> Homo sapiens

<400> 409  
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cagcatttaa tgaaaaatth atgcttaaga agtaaaaatg gcaggcttcc 150  
tagataatth tcgttgcca gaatgtgaat gtattgactg gagtgagaga 200  
agaaatgctg tggcatctgt tgtcgcaggt atattgtttt ttacaggctg 250  
gtggataatg attgatgcag ctgtggtgta tctaagcca gaacagttga 300  
accatgcctt tcacacatgt ggtgtattht ccacattggc thcttcatg 350  
ataaatgctg tatccaatgc tcaggtgaga ggtgatagct atgaaagcgg 400  
ctgtttagga agaacagggt ctogagtttg gctthtcatg ggtthcatgt 450  
tgatgtttgg gtcacttatt gcttccatgt ggattcttht tgggtcatat 500  
gttaccctaaa atactgatgt ttatccggga ctagctgtgt thtttcaaaa 550



Ser Asn Ala Gln Val Arg Gly Asp Ser Tyr Glu Ser Gly Cys Leu  
80 85 90

Gly Arg Thr Gly Ala Arg Val Trp Leu Phe Ile Gly Phe Met Leu  
95 100 105

Met Phe Gly Ser Leu Ile Ala Ser Met Trp Ile Leu Phe Gly Ala  
110 115 120

Tyr Val Thr Gln Asn Thr Asp Val Tyr Pro Gly Leu Ala Val Phe  
125 130 135

Phe Gln Asn Ala Leu Ile Phe Phe Ser Thr Leu Ile Tyr Lys Phe  
140 145 150

Gly Arg Thr Glu Glu Leu Trp Thr  
155

<210> 411  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 411  
gtttgaggaa gctgggatac 20

<210> 412  
<211> 20  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-20  
<223> Synthetic construct.

<400> 412  
ccaaactcga gcacctgttc 20

<210> 413  
<211> 40  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-40  
<223> Synthetic construct.

<400> 413  
atggcaggct tcctagataa ttttcgttgg ccagaatgtg 40

<210> 414

<211> 1337  
<212> DNA  
<213> Homo sapiens

<400> 414

gttgatggca aacttcctca aaggaggggc agagcctgcg cagggcagga 50  
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actgcatcta gaggagggcc gtctgtgagg ccactacccc tccagcaact 150  
gggaggtggg actgtcagaa gctggcccag ggtggtggtc agctgggtca 200  
gggacctacg gcacctgctg gaccacctcg ccttctccat cgaagcaggg 250  
aagtgggagc ctcgagccct cgggtggaag ctgaccccaa gccacccttc 300  
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tttgccatag tcacgacatg gatgtttatt cgaagctaca tgagcttcag 400  
catgaaaacc atccgtctgc cacgctggct ggcagcctcg cccaccaagg 450  
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aactactttg cgtttaaaat ctgcagtggg gccgccaacg tcgtgggccc 550  
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tgggcagagg cctaaacatc gccctggtga atggaaccac gggagctgtg 650  
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gacttgggga gttcctacgc aaaacaactg ggcttcggg acagctgggt 850  
cttcatagga gccaaagacc tcaggggtaa aagccccttt gagcagttct 900  
taaagaacag ccagacaca aacaaatag agggatggcc agagctgctg 950  
gagatggagg gctgcatgcc cccgaagcca ttttaggggtg gctgtggctc 1000  
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cccggcaggg gctgaggagg aggagcaggg ggtgctgctt ggaaggtgct 1100  
gcaggtcctt gcacgctgtg tcgcgcctct cctcctcgga aacagaaccc 1150  
tcccacagca catcctaccc ggaagaccag cctcagaggg tccttctgga 1200  
accagctgtc tgtggagaga atgggggtgct ttcgtcaggg actgctgacg 1250  
gctggtcctg aggaaggaca aactgccag acttgagccc aattaaattt 1300  
tatttttgcg ggttttgaaa aaaaaaaaaa aaaaaaa 1337

<210> 415  
 <211> 224  
 <212> PRT  
 <213> Homo sapiens

<400> 415  
 Met Arg Val Ser Gly Val Leu Arg Leu Leu Ala Leu Ile Phe Ala  
 1 5 10 15  
 Ile Val Thr Thr Trp Met Phe Ile Arg Ser Tyr Met Ser Phe Ser  
 20 25 30  
 Met Lys Thr Ile Arg Leu Pro Arg Trp Leu Ala Ala Ser Pro Thr  
 35 40 45  
 Lys Glu Ile Gln Val Lys Lys Tyr Lys Cys Gly Leu Ile Lys Pro  
 50 55 60  
 Cys Pro Ala Asn Tyr Phe Ala Phe Lys Ile Cys Ser Gly Ala Ala  
 65 70 75  
 Asn Val Val Gly Pro Thr Met Cys Phe Glu Asp Arg Met Ile Met  
 80 85 90  
 Ser Pro Val Lys Asn Asn Val Gly Arg Gly Leu Asn Ile Ala Leu  
 95 100 105  
 Val Asn Gly Thr Thr Gly Ala Val Leu Gly Gln Lys Ala Phe Asp  
 110 115 120  
 Met Tyr Ser Gly Asp Val Met His Leu Val Lys Phe Leu Lys Glu  
 125 130 135  
 Ile Pro Gly Gly Ala Leu Val Leu Val Ala Ser Tyr Asp Asp Pro  
 140 145 150  
 Gly Thr Lys Met Asn Asp Glu Ser Arg Lys Leu Phe Ser Asp Leu  
 155 160 165  
 Gly Ser Ser Tyr Ala Lys Gln Leu Gly Phe Arg Asp Ser Trp Val  
 170 175 180  
 Phe Ile Gly Ala Lys Asp Leu Arg Gly Lys Ser Pro Phe Glu Gln  
 185 190 195  
 Phe Leu Lys Asn Ser Pro Asp Thr Asn Lys Tyr Glu Gly Trp Pro  
 200 205 210  
 Glu Leu Leu Glu Met Glu Gly Cys Met Pro Pro Lys Pro Phe  
 215 220

<210> 416  
 <211> 21  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence

<222> 1-21  
<223> Synthetic construct.

<400> 416  
gccatagtca cgacatggat g 21

<210> 417  
<211> 18  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-18  
<223> Synthetic construct.

<400> 417  
ggatggccag agctgctg 18

<210> 418  
<211> 26  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-26  
<223> Synthetic construct.

<400> 418  
aaagtacaag tgtggcctca tcaagc 26

<210> 419  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 419  
tctgactcct aagtcaggca ggag 24

<210> 420  
<211> 24  
<212> DNA  
<213> Artificial

<220>  
<221> Artificial Sequence  
<222> 1-24  
<223> Synthetic construct.

<400> 420  
attctctcca cagacagctg gttc 24

<210> 421  
 <211> 46  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-46  
 <223> Synthetic construct.

<400> 421  
 gtacaagtgt ggcctcatca agccctgccc agccaactac tttgcg 46

<210> 422  
 <211> 1701  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <221> unsure  
 <222> 1528  
 <223> unknown base

<400> 422  
 gagactgcag agggagataa agagagaggg caaagaggca gcaagagatt 50  
 tgtcctgggg atccagaaac ccatgatacc ctactgaaca ccgaatcccc 100  
 tggaagccca cagagacaga gacagcaaga gaagcagaga taaatacaact 150  
 cacgccagga gctcgtctgc tctctctctc tctctctcac tctcctctcc 200  
 ctctctctct gctgtctcta gtcctctagt cctcaaattc ccagtccctc 250  
 gcacccttct ctgggacact atgttggtct cgcctctcct gctggagggtg 300  
 atttgatcc tggctgcaga tgggggtcaa cactggacgt atgaggggcc 350  
 acatgggtcag gaccattggc cagcctctta ccctgagtgt ggaaacaatg 400  
 cccagtgcgc catcgatatt cagacagaca gtgtgacatt tgaccctgat 450  
 ttgcctgctc tgcagcccca cggatatgac cagcctggca ccgagccttt 500  
 ggacctgcac aacaatggcc acacagtga actctctctg ccctctaccc 550  
 tgtatctggg tggacttccc cgaaaatatg tagctgcca gctccacctg 600  
 cactgggggtc agaaaggatc ccagggggg tcagaacacc agatcaacag 650  
 tgaagccaca tttgcagagc tccacattgt acattatgac tctgattcct 700  
 atgacagctt gagtgaggct gctgagaggc ctcagggcct ggctgtcctg 750  
 ggcatcctaa ttgagggtgg tgagactaag aatatagctt atgaacacat 800  
 tctgagtcac ttgcatgaag tcaggcataa agatcagaag acctcagtgc 850



ctcccttcaa cctaagagag ctgctcccca aacagctggg gcagtacttc 900  
cgctacaatg gctcgctcac aactccccct tgctaccaga gtgtgctctg 950  
gacagttttt tatagaaggt cccagatttc aatggaacag ctggaaaagc 1000  
ttcaggggac attgttctcc acagaagagg agccctctaa gcttctggta 1050  
cagaactacc gagcccttca gcctctcaat cagcgcatgg tctttgcttc 1100  
tttcatccaa gcaggatcct cgtataccac aggtgaaatg ctgagtctag 1150  
gtgtaggaat cttggttggc tgtctctgcc ttctcctggc tgtttatttc 1200  
attgctagaa agattcggaa gaagaggctg gaaaaccgaa agagtgtggt 1250  
cttcacctca gcacaagcca cgactgaggc ataaattcct tctcagatac 1300  
catggatgtg gatgacttcc cttcatgcct atcaggaagc ctctaaaatg 1350  
gggtgtagga tctggccaga aacactgtag gagtagtaag cagatgtcct 1400  
ccttccccctg gacatctctt agagaggaat ggaccagggc tgtcattcca 1450  
ggaagaactg cagagccttc agcctctcca aacatgtagg aggaaatgag 1500  
gaaatcgctg tgttgtaaat gcagaganca aactctgttt agttgcaggg 1550  
gaagtttggg atatacccca aagtcctcta cccctcact tttatggccc 1600  
tttccctaga tatactgagg gatctctcct taggataaag agttgctggt 1650  
gaagttgtat atttttgatc aatatatttg gaaattaaag tttctgactt 1700  
t 1701

<210> 423  
<211> 337  
<212> PRT  
<213> Homo sapiens

<400> 423  
Met Leu Phe Ser Ala Leu Leu Leu Glu Val Ile Trp Ile Leu Ala  
1 5 10 15  
Ala Asp Gly Gly Gln His Trp Thr Tyr Glu Gly Pro His Gly Gln  
20 25 30  
Asp His Trp Pro Ala Ser Tyr Pro Glu Cys Gly Asn Asn Ala Gln  
35 40 45  
Ser Pro Ile Asp Ile Gln Thr Asp Ser Val Thr Phe Asp Pro Asp  
50 55 60  
Leu Pro Ala Leu Gln Pro His Gly Tyr Asp Gln Pro Gly Thr Glu  
65 70 75  
Pro Leu Asp Leu His Asn Asn Gly His Thr Val Gln Leu Ser Leu

80	85	90
Pro Ser Thr Leu Tyr 95	Leu Gly Gly Leu Pro Arg Lys Tyr Val 100	Ala 105
Ala Gln Leu His 110	Leu His Trp Gly Gln Lys Gly Ser Pro Gly 115	Gly 120
Ser Glu His Gln 125	Ile Asn Ser Glu Ala Thr Phe Ala Glu Leu 130	His 135
Ile Val His Tyr 140	Asp Ser Asp Ser Tyr Asp Ser Leu Ser Glu 145	Ala 150
Ala Glu Arg Pro 155	Gln Gly Leu Ala Val Leu Gly Ile Leu Ile 160	Glu 165
Val Gly Glu Thr 170	Lys Asn Ile Ala Tyr Glu His Ile Leu Ser 175	His 180
Leu His Glu Val 185	Arg His Lys Asp Gln Lys Thr Ser Val Pro 190	Pro 195
Phe Asn Leu Arg 200	Glu Leu Leu Pro Lys Gln Leu Gly Gln Tyr 205	Phe 210
Arg Tyr Asn Gly 215	Ser Leu Thr Thr Pro Pro Cys Tyr Gln Ser 220	Val 225
Leu Trp Thr Val 230	Phe Tyr Arg Arg Ser Gln Ile Ser Met Glu 235	Gln 240
Leu Glu Lys Leu 245	Gln Gly Thr Leu Phe Ser Thr Glu Glu Glu 250	Pro 255
Ser Lys Leu Leu 260	Val Gln Asn Tyr Arg Ala Leu Gln Pro Leu 265	Asn 270
Gln Arg Met Val 275	Phe Ala Ser Phe Ile Gln Ala Gly Ser Ser 280	Tyr 285
Thr Thr Gly Glu 290	Met Leu Ser Leu Gly Val Gly Ile Leu Val 295	Gly 300
Cys Leu Cys Leu 305	Leu Leu Ala Val Tyr Phe Ile Ala Arg Lys 310	Ile 315
Arg Lys Lys Arg 320	Leu Glu Asn Arg Lys Ser Val Val Phe Thr 325	Ser 330
Ala Gln Ala Thr 335	Thr Glu Ala	

<210> 424  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 424  
 gtaaagtcgc tggccagc 18

<210> 425  
 <211> 18  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-18  
 <223> Synthetic construct.

<400> 425  
 cccgatctgc ctgctgta 18

<210> 426  
 <211> 24  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-24  
 <223> Synthetic construct.

<400> 426  
 ctgcactgta tggccattat tgtg 24

<210> 427  
 <211> 45  
 <212> DNA  
 <213> Artificial

<220>  
 <221> Artificial Sequence  
 <222> 1-45  
 <223> Synthetic construct.

<400> 427  
 cagaaaccca tgatacccta ctgaacaccg aatcccctgg aagcc 45

<210> 428  
 <211> 1073  
 <212> DNA  
 <213> Homo sapiens

<400> 428  
 aatttttcac cagagtaaac ttgagaaacc aactggacct tgagtattgt 50  
 acattttgcc tcgtggaccc aaaggtagca atctgaaaca tgaggagtac 100  
 gattctactg ttttgtcttc taggatcaac tcggtcatta ccacagctca 150

aacctgctttt gggactccct cccacaaaac tggctccgga tcagggaaca 200  
 ctaccaaacc aacagcagtc aaatcaggtc tttccttctt taagtctgat 250  
 accattaaca cagatgctca cactggggcc agatctgcat ctgttaaatac 300  
 ctgctgcagg aatgacacct ggtaccaga cccaccatt gaccctggga 350  
 gggttgaatg tacaacagca actgcacca catgtgttac caatttttgt 400  
 cacacaactt ggagcccagg gcactatcct aagctcagag gaattgccac 450  
 aaatcttcac gagcctcacc atccattcct tgttcccggg aggcaccttg 500  
 cccaccagtc aggcaggggc taatccagat gtccaggatg gaagccttcc 550  
 agcaggagga gcagggtgaa atcctgccac ccagggaacc ccagcaggcc 600  
 gcctcccaac tcccagtggc acagatgacg actttgcagt gaccaccct 650  
 gcaggcatcc aaaggagcac acatgccatc gaggaagcca ccacagaatac 700  
 agcaaatgga attcagtaag ctgtttcaaa ttttttcaac taagctgcct 750  
 cgaatttggg gatacatgtg aatctttatc attgattata ttatggaata 800  
 gattgagaca cattggatag tottagaaga aattaattct taatttacct 850  
 gaaaatattc ttgaaatttc agaaaatatg ttctatgtag agaatcccaa 900  
 cttttaaaaa caataattca atggataaat ctgtctttga aatataacat 950  
 tatgtgcct ggatgatatg catattaaaa catatttgga aaactggaaa 1000  
 aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa aaaaaaaaaa 1050  
 aaaaaaaaaa aaaaaaaaaa aaa 1073

<210> 429  
 <211> 209  
 <212> PRT  
 <213> Homo sapiens

<400> 429  
 Met Arg Ser Thr Ile Leu Leu Phe Cys Leu Leu Gly Ser Thr Arg  
 1 5 10 15  
 Ser Leu Pro Gln Leu Lys Pro Ala Leu Gly Leu Pro Pro Thr Lys  
 20 25 30  
 Leu Ala Pro Asp Gln Gly Thr Leu Pro Asn Gln Gln Gln Ser Asn  
 35 40 45  
 Gln Val Phe Pro Ser Leu Ser Leu Ile Pro Leu Thr Gln Met Leu  
 50 55 60  
 Thr Leu Gly Pro Asp Leu His Leu Leu Asn Pro Ala Ala Gly Met  
 65 70 75

Thr	Pro	Gly	Thr	Gln	Thr	His	Pro	Leu	Thr	Leu	Gly	Gly	Leu	Asn
				80					85					90
Val	Gln	Gln	Gln	Leu	His	Pro	His	Val	Leu	Pro	Ile	Phe	Val	Thr
				95					100					105
Gln	Leu	Gly	Ala	Gln	Gly	Thr	Ile	Leu	Ser	Ser	Glu	Glu	Leu	Pro
				110					115					120
Gln	Ile	Phe	Thr	Ser	Leu	Ile	Ile	His	Ser	Leu	Phe	Pro	Gly	Gly
				125					130					135
Ile	Leu	Pro	Thr	Ser	Gln	Ala	Gly	Ala	Asn	Pro	Asp	Val	Gln	Asp
				140					145					150
Gly	Ser	Leu	Pro	Ala	Gly	Gly	Ala	Gly	Val	Asn	Pro	Ala	Thr	Gln
				155					160					165
Gly	Thr	Pro	Ala	Gly	Arg	Leu	Pro	Thr	Pro	Ser	Gly	Thr	Asp	Asp
				170					175					180
Asp	Phe	Ala	Val	Thr	Thr	Pro	Ala	Gly	Ile	Gln	Arg	Ser	Thr	His
				185					190					195
Ala	Ile	Glu	Glu	Ala	Thr	Thr	Glu	Ser	Ala	Asn	Gly	Ile	Gln	
				200					205					

<210> 430  
 <211> 1257  
 <212> DNA  
 <213> Homo Sapien

<400> 430  
 ggagagagggc gcgcgggtga aaggcgcatt gatgcagcct gcggcggcct 50  
 cggagcgcgg cggagccaga cgctgaccac gttcctctcc tcggtctcct 100  
 ccgcctccag ctccgcgctg cccggcagcc gggagccatg cgaccccagg 150  
 gcccgcgcgc ctcccgcag cggctccgcg gcctcctgct gctcctgctg 200  
 ctgcagctgc ccgcgcgcgc gagcgcctct gagatcccca aggggaagca 250  
 aaaggcgcag ctccggcaga gggaggtggt ggacctgtat aatggaatgt 300  
 gcttacaagg gccagcagga gtgcctggtc gagacgggag ccctggggcc 350  
 aatgttattc cgggtacacc tgggatccca ggtcgggatg gattcaaagg 400  
 agaaaagggg gaatgtctga gggaaagctt tgaggagtcc tggacacca 450  
 actacaagca gtgttcattg agttcattga attatggcat agatcttggg 500  
 aaaattgcgg agtgtacatt tacaagatg cgttcaaata gtgctctaag 550  
 agttttgttc agtggtcac ttcggtctaa atgcagaaat gcatgctgtc 600  
 agcgttggtg tttcacattc aatggagctg aatgttcagg acctcttccc 650

attgaagcta taatttattt ggaccaagga agccctgaaa tgaattcaac 700  
aattaatatt catcgactt cttctgtgga aggactttgt gaaggaattg 750  
gtgctggatt agtggatggt gctatctggg ttggcacttg ttcagattac 800  
ccaaaaggag atgcttctac tggatggaat tcagtttctc gcatcattat 850  
tgaagaacta ccaaaataaa tgctttaatt ttcatttgct acctcttttt 900  
ttattatgcc ttggaatggt tcacttaaat gacattttta ataagtttat 950  
gtatacatct gaatgaaaag caaagctaaa tatgtttaca gaccaaagtg 1000  
tgatttcaca ctgtttttta atctagcatt attcattttg cttcaatcaa 1050  
aagtggtttc aatatttttt ttagttgggt agaatacttt cttcatagtc 1100  
acattctctc aacctataat ttggaatatt gttgtggtct tttgtttttt 1150  
ctcttagtat agcattttta aaaaaatata aaagctacca atctttgtac 1200  
aatttgtaaa tgtaagaat tttttttata tctgttaaatt aaaaattatt 1250  
tccaaca 1257

<210> 431  
<211> 243  
<212> PRT  
<213> Homo Sapien

<400> 431  
Met Arg Pro Gln Gly Pro Ala Ala Ser Pro Gln Arg Leu Arg Gly  
1 5 10 15  
Leu Leu Leu Leu Leu Leu Leu Gln Leu Pro Ala Pro Ser Ser Ala  
20 25 30  
Ser Glu Ile Pro Lys Gly Lys Gln Lys Ala Gln Leu Arg Gln Arg  
35 40 45  
Glu Val Val Asp Leu Tyr Asn Gly Met Cys Leu Gln Gly Pro Ala  
50 55 60  
Gly Val Pro Gly Arg Asp Gly Ser Pro Gly Ala Asn Val Ile Pro  
65 70 75  
Gly Thr Pro Gly Ile Pro Gly Arg Asp Gly Phe Lys Gly Glu Lys  
80 85 90  
Gly Glu Cys Leu Arg Glu Ser Phe Glu Glu Ser Trp Thr Pro Asn  
95 100 105  
Tyr Lys Gln Cys Ser Trp Ser Ser Leu Asn Tyr Gly Ile Asp Leu  
110 115 120  
Gly Lys Ile Ala Glu Cys Thr Phe Thr Lys Met Arg Ser Asn Ser  
125 130 135

Ala	Leu	Arg	Val	Leu	Phe	Ser	Gly	Ser	Leu	Arg	Leu	Lys	Cys	Arg	140	145	150
Asn	Ala	Cys	Cys	Gln	Arg	Trp	Tyr	Phe	Thr	Phe	Asn	Gly	Ala	Glu	155	160	165
Cys	Ser	Gly	Pro	Leu	Pro	Ile	Glu	Ala	Ile	Ile	Tyr	Leu	Asp	Gln	170	175	180
Gly	Ser	Pro	Glu	Met	Asn	Ser	Thr	Ile	Asn	Ile	His	Arg	Thr	Ser	185	190	195
Ser	Val	Glu	Gly	Leu	Cys	Glu	Gly	Ile	Gly	Ala	Gly	Leu	Val	Asp	200	205	210
Val	Ala	Ile	Trp	Val	Gly	Thr	Cys	Ser	Asp	Tyr	Pro	Lys	Gly	Asp	215	220	225
Ala	Ser	Thr	Gly	Trp	Asn	Ser	Val	Ser	Arg	Ile	Ile	Ile	Glu	Glu	230	235	240

Leu Pro Lys

<210> 432  
 <211> 18  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Artificial Sequence

<400> 432  
 aggacttgcc ctcaggaa 18

<210> 433  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 433  
 cgcaggacag ttgtgaaaat a 21

<210> 434  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Synthetic oligonucleotide probe

<400> 434  
 atgacgctcg tccaaggcca c 21

<210> 435

<211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 435  
 cccacctgta ccaccatgt 19  
  
 <210> 436  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 436  
 actccaggca ccatctgttc tccc 24  
  
 <210> 437  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 437  
 aagggctggc attcaagtc 19  
  
 <210> 438  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 438  
 tgacctggca aaggaagaa 19  
  
 <210> 439  
 <211> 21  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> Synthetic oligonucleotide probe  
  
 <400> 439  
 cagccaccct ccagtccaag g 21  
  
 <210> 440  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence



<220>  
<223> Synthetic oligonucleotide probe

<400> 440  
gggtcgtggtt ttggagaga 19

<210> 441  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 441  
ctggccctca gagcaccaat 20

<210> 442  
<211> 25  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 442  
tcctccatca cttcccctag ctcca 25

<210> 443  
<211> 24  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 443  
ctggcaggag ttaaagttcc aaga 24

<210> 444  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 444  
aaaggacacc gggatgtg 18

<210> 445  
<211> 26  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 445  
agcgtacact ctctccaggc aaccag 26

<210> 446  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 446  
caattctgga tgaggtggta ga 22

<210> 447  
<211> 20  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 447  
caggactgag cgcttggtta 20

<210> 448  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 448  
caaagcgcca agtaccggac c 21

<210> 449  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 449  
ccagacctca gccaggaa 18

<210> 450  
<211> 18  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Synthetic oligonucleotide probe

<400> 450  
ccctagctga ccccttca 18



<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 456

ccttgaaaag gacccagttt 20

<210> 457

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 457

atgagtcgca cctgctgttc cc 22

<210> 458

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 458

tagcagctgc ccttggtta 18

<210> 459

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 459

aacagcaggt gcgactcatc ta 22

<210> 460

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 460

tgctaggcga cgacacccag acc 23

<210> 461

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 461

tggacacgtg gcagtgga 18

<210> 462

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 462

tcatggtctc gtccattc 19

<210> 463

<211> 27

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 463

caccatttgt ttctctgtct ccccatc 27

<210> 464

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 464

ccggcatcct tggagtag 18

<210> 465

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 465

tccccattag cacaggagta 20

<210> 466

<211> 23

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 466

aggctcttgc ctgtcctgct gct 23

<210> 467

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 467

gcccagagtc ccacttgt 18

<210> 468

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 468

actgctccgc ctactacga 19

<210> 469

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 469

aggcatcctc gccgtcctca 20

<210> 470

<211> 19

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 470

aaggccaagg tgagtccat 19

<210> 471

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> Synthetic oligonucleotide probe

<400> 471

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